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Fig. 1A

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HCV-1	l a	1 ATGAGCACGA	ል ሞርርጥአ አ	አ <i>ርር</i> ሞሮ፣		7 7 7 C 7			50
HCV-J	i b	A	TICCIAA	ACC1CA	MAAAAA	AAACA	AACGTAA	CACCAACC	G
HCG9	10					0			
BNL1	16								-
BNL2	10				6				-
CAM1078	1 =				G				-
FR2	1 f				·G		<u>A</u> -A		
	4.1					0	C		-
HC-J6	2=				~	_			
HC-J8	2h	<u>n</u>			·G	0	A-A		
S83	20	A			·G	0	A-A	A	-
NE 92	24	A			G	0	A-A	T	-
FR4	24	A				C	A-A	T	
ENL4	2.	A			G	CT-	A-A	T	-
ENL5	25	<u>A</u>			G	C	A-A	[_
ENTO	· Zn	<u>V</u>			G	C	A-A	<u>T</u>	-
1707 1	_								
NZL1	3a	AC	[G	C	A-A	T	_
HCV-TR	35	AC	['		G-C	C	2-2	DCT	_
NE48	3C	AC	[' <u>A</u> '	C	G		2-2	T	
NE274	3a	AC	[A	C 			2-2	T	_
NE145	3e	AC3	[A	C			4-4	CT	
NE125	3f	AT1	·		G-C	-cc	-A-A	200	_
Z 4	4 a				G				_
Z1	4b	A			6				_
GB358	4 c				6				_
DK13	4d				6	C			_
GB809	4e			T	6				_
BNL7	4 k			·	G				_
					G				-
3E95	5a					_	70 70		
	•				G		-A-A		-
EK2	6а	ACT	7			_			

FR1	7 =	ACT	70	_	_	_			
- 11.									
VN4	0 -	ACT	_	_					
VN13	σa	AC1	A	C	G- <i></i> -	-C	-A-A	T	-
ANTZ	ag	ACT			G	-C	A		-
VN12	9a	ACT	<u>A</u>	c	G	-C	-A-A	n	-
NE98	10a	ACT		A	G	-c	-A-A	N	ī
						_		-11	•



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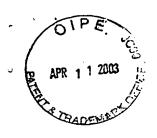
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Fig.1B

HCV-1	1 -	51 TCGCCCACAGGAC	יכייר א אפייירררפ	:	CCTCACAT	100
HCV-J		C				
HC-G9		C				
BNL1		CTK-GS				
BNL2		C				
CAM1078		C				
FR2	11	C	1			
	_	_	_ ~	~	_	_
HC-J6		<u>A</u>				
HC-J8		C				
s83		C				
NE92	2d	C		CT	'C	
FR4	2f		T	C	C	C
BNL3	2e	C		C	C	C
BNL5		C				
NZL1	3a				A	
HCV-TR		A				
NE48						
NE274						
NE145		GA				
NE125		C				
NEIZJ	J.			· -	. •	
2.4	4 a	CCAT	4	т	'C	C
21		CATT				
GB358		CCAT				
		CAT				
DK13						
GB809	4 e	CCAT	·T	1		
BNL7	4 K	CCAT	T'	1		C
BE95	5a			C1		C
HK2	6a	AC				C
FR1	7a	TAT		C	c	
VN4 VN13	8a 85	C			C	
4111J	UD					
VN12	9a	ATT	[- C		
NE98	10a	CG	T	4 - -C		



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Fig.1C

HCV-1	101 La TTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGC	
HCV-J HC-G9	1bC	ŢG
BNL1	1cG	G
BNL1 BNL2	_dC	TG
CAM1078	le -CGC-A	»ccc
FR2	1fCG	AGC-G
HC-J6	2a -A	<i>\</i>
HC-J8	2bC	AG
S83	2c -AC	
NE92	2d -ACC-G	G
FR4	2fCG	G
BNL3	2eC	C-AG
BNL5	2h -ACC-G	
NZL1	3a -AGACAC	r
HCV-TR	3b -ATGCTAC	AGTAC-T
NE48	3c -AGCTCT	TAC-T
NE274	3d -CACAA	AGTTC-T
NE145	3e -AACAC	ATC-T
NE125	3f -AG-AACAC	AGT-C-T
24	4aCG	TC
21	4bC	AG-TC-G
GB358	4c	TG
DK13	4d	TG
GB809	4e	TC-G
BNL7	4kCG	TC-G
שמפ	E	
BE95	5aGA	TC-G
HK2	6-	
ΠΛΖ	6a	
FR1	7a	
FKI	/a	
VN4	Яз -СС	
VN13	8a -CC	

VN12	9a -CAAC-T	
3	** AC 1	·
NE98	10aGC-AA	-TAGT-C-C
		0



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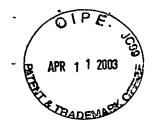
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Fig.1D

HCV-1 HCV-J	1a 1b	151 AAGACTTC	CGAGCGG'	rcgc:	AAC	CTC(GAG(GTAC	SAC	GTC#	GCC,	TATC	-cc	00 <u>A</u>
HC-G9 BNL1	lç						-C	-G	-G-			T		_
BNL2	. 9			<u>A</u>			-T	-C	-G	- <u>A</u>				-
CAM1078			G~====				- T - <i>I</i>	AC	-G-:	- <u>A</u>		T	$-\mathrm{T}$	-
FR2	1f							- A	-G-	-D	-A	T		-
							_		G-	- 				-
HC-J6	2a		G	C-	-G-	- <u>A</u>	-T	-A	-G	-C		C	T-	_
HC-J8	2b		T <u>A</u> -	C-	-G-	-G	-T	-AC-		-C		C	G-	_
S83	2c	A	<u>A</u>	C-	-G-	-A	-T	-G	-G			^ -	T-	_
NE92	2d	A		C	-G-	- A	- T	-G	-G			^		_
FR4	2f		TA	C-	-G-	- <u>Z</u>	- T	-A	-G	-c			A -	_
BNL3	Ze		TA	C-	-G-	- A	- T	- A	·c			^	T-	_
BNL5	2h	A	A	C-	-G-	- <u>A</u>	- T	-G	-G	-C	(:	T-	_
NIGT 3	2 -	70		_	_									
NZL1 HCV-TR	32	A	T <u>A</u>	A	-G-		-C	-AC-		-¥				_
NE48	35				-G-		-CAA	AACA	۲G~-		C-T-			-
NE 4 5 NE 2 7 4	20			<u>A</u>	-G-	- -	-C-C	CGC-	·G	-G				
NE145	30	A		<u>A</u> G-		-C	-CAF	/CC-	·G	-G				_
NE125	36		A	A		-C	-C	-AC-	·G~-	- <u>A</u>		T-		-
NEIZJ	21	AT					-C	AC-	·G	-G				-
Z.4	4 a		G				ጥ	. C	_		7			
Z1	4 b		G	A			· T — -	.c	C		A			-
GB358	4 C						т -т							_
DK13	4 d		- G				T	.G	c					_
GB809	4 e		- G 				·Ť	·G	G	-C	D			_
BNL7	4 k		- G 				·T	·G		-C	Δ			_
		•												
BE95	5 a		GA			-c	T	AC-	G			T-		_
HK2	6a		A	C	-G	-CA-		·C	G	-C	A	<u>A</u> -	- <u>A</u>	_
FR1	7 a	C	A	c	-G	A		C	G	-C	0	<u>A</u> -	- <u>A</u>	_
	_													
VN4	8a		ra	C	-G	-CA-			G	·C	<u>AA</u>	A-		-
VN13	86	A	A	C	-G	-CA-	G			·C	A	<u>A</u> -	-G	-
TD110	•	_		_	_									
VN12	9a	(5A	-C	-GG-	-CA-			G	C	<u>44</u>	A-		-
NE98	10-								_	_	_			
MESC	102						CA-		G	C	AC		G	}



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Fig.1E

HCV-1 HCV-J HC-G9 BNL1 BNL2 CAM1078 FR2	201 250 1a GGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGC 1b
HC-J6 HC-J8 S83 NE92 FR4 BNL3 BNL5	2aAGCTACTAATGAA-AAAC 2b A-AGCTACCA-TGAAAAT 2c A-AGCAACTA-TGAAGAAA 2d A-AGCGACTA-TGAA-AAAA
NZL1 HCV-TR NE48 NE274 NE145 NE125	3a GAGAC-T
Z4 Z1 GB358 DK13 GB809 BNL7	4a GC-AAATG
BE95	5aGC-AACCTGA
нк2	6aGC-ACA
FR1	7aTAC-AGACAC-T-GGAC
VN4 VN13	8a A-TGC-AC-AAACC-TCC 8bTGAC-AAACC-TA
VN12	9aTGC-A-AA-C-AC-ATTC
NE98	10aGCAATT



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Fig.1F

HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	16 1d 1d	251 CCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGATGGCTCCTGTC CCTATGAN	A C C
HC-J6 HC-J8 S83 NE92 FR4 BNL3 BNL5	2a 2b 2c 2d 2f 2e	AA-C-GACTCA	C C C C
NZL1 HCV-TR NE48 NE274 NE145 NE125	3b 3c 3d 3e	ATCAG	C C C
24 21 GB358 DK13 GB809 BNL7	40 40 4d 4e	A	ў ўТ ХТ
BE95	5a	TC-CCT <u>A</u> GG	T
HK2		-TTACTATC	
FR1		TCAC	
VN4 VN13	8a 8b	-TTA	: :
VN12		TGC	
NE98	10a	AG	G



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Fig.1G

HCV-1	la	301 CGTGGCTCTCGGCCTAGCT	GGGGCCCCACAGA	350 CCCCCGGCGTAGGTCGCG
HCV-J HC-G9 BNL1 BNL2	lc ld ld	CT-	TT-T	
FR2	1f	CCT	T <u>A</u>	<u>y</u> <u>y</u>
HC-J6 HC-J8	2b	<u>A</u> TCTCTCT-	C	<u>V</u> V
S83 NE92		CTCTCA-		
FR4 BNL3 BNL5	2f 2e	G		
NZL1		CCTATC		
HCV-TR NE48		TT-		
NE274		CATCT-		
NE145		CCAGT-		
NE125	3f		TA-A	
Z 4		CATCT-		
Z1		CTCAGTCT-		
GB358 DK13		AGTCT-		
GB809		CGGTCT-		
BNL7		CT		
BE95		AAT-		
HK2	6a	CCACAT-	AT	C-AC
FR1	7a	CGAT-	AC	AC
VN4 VN13	8a 8b	CCAT-	A-AC	C N-GC
VN12	9a	CGGA	AT	N-GC
NE98	10a	C		



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Fig.1H

HCV-1 HCV-J HC-G9 FR2	351 la CAATTTGGGTAAGGTCATCGATACCC lb T lc lf	A
HC-J6 HC-J8 583 NE92 FR4 BNL3	2aCG	TTT
NZL1 HCV-TR NE48 NE274 NE145 NE125	3a	-AT-A
Z4 Z1 GB358 DK13 GB809	4aC	-GT
BE95	5a T	-AT
HK2	6a G	-ATGT
FR1	7aC	A-NNC- <u>A</u>
VN4 VN13	8aC	TN-S
VN12	9aCC	-СТ



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Fig.1I

HCV-1 HCV-J HC-G9 FR2	401 450 la TGGGGTACATACCGCTCGTCGGCGCCCCTCTTGGAGGCGCTGCCAGGGCC lb
HC-J6 HC-J8 S83 NE92 FR4 BNL3	2a
NZL1 HCV-TR NE48 NE274 NE145 NE125	3a CTCAATCAA 3b TCAA
Z4 Z1 GB358 DK13 GB809	4a ACAG
BE95	5aTCAGCAGTCAT
HK2	6aTCGGGT-GCTCGGCTG
FR1	7aTGC-AA-GGGCTGGCT
VN4 VN13	8aTCTGATGW-GTCGGN 8b -A-AT
VN12	9aATGTCTGGCAA





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Fig.1J

HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	1b 1c 1d 1d	451 500 CTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAGGATTA-ACTCN-AT
HC-J6 HC-J8 S83 NE92 BNL3 FR4 BNL4 BNL5 BNL6	2b 2c 2d	C
NZL1 HCV-TR NE48 NE274 NE145 NE125	3b 3c 3d 3e	C
Z4 Z1 GB358 DK13 GB809 BNL7 SNL8 SNL9 BNL10 BNL11 SNL12	4b	
BE95	5a	CACTGACTGGA
HK2	6a	CAGACAA-CGGA-CT
FR1	7a	TACAA-CGGCTC
VN4	8a	TNA-TCN
VN12	9a	NATACCA-CGGA-A
NE 95	10a	AA-TT-TC





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Fig.1K

		•	
		501 550	Λ
HCV-1	1 -	GAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCCCTGCTCTCTT	U
HCV-J		TGCG	
HC-G9	lc	T-GCTTAC-	
BNL1	1d	T-GCGC-	
BNL2	1d	TT-GCT-ATT-TGC-	
FR2	1 f	NNT-A	
\-		K C1 - NI R	
	_		
HC-J6	2a	T-ACT-G	
HC-J8	2b	TT-ACTT-GTTGA-	
S83	2 c	TT-GC	
NE92		T-GCT-ATA	
BNL3			
		TNGTT-T-G	
FR4		T-GCCTT-GTCT-G	
BNL4	2α	TGTGTGTTG	
BNL5		TGCT-GTAC-	
BNL6	21	GT-AT-AT-A	
NZL1	3a	T-GCCTTTTT	
HCV-TR		TCTCCTC-	
NE48		TT-A	
NE274		TT-ACT-GTTT	
NE145			
NE125	3f	TT-GCC-TTTCTA-	
24	4 =	TCTATTG-	
21		TA-TG-	
-			
GB358		<u>T</u> <u>C</u>	
DK13		TC	
GB809	4 e	TCC	
BNL7		CC	
BNL8		CTAC	
BNL9		TCTATG-	
BNL10	4 k	TACYT	
BNL11	4 k	YCCTCTATG-	
BNL12		A-CA-TG-	
DIVIDIZ		z c	
05	_		
BE95	5a	$\underline{\mathtt{T}} \mathbf{T} - \underline{\mathtt{A}} - \underline{\mathtt{C}}\underline{\mathtt{T}} - \underline{\mathtt{A}}\underline{\mathtt{T}} - \underline{\mathtt{T}} - \underline{\mathtt{T}} - \underline{\mathtt{T}} - \underline{\mathtt{T}} - \underline{\mathtt{T}} - \underline{\mathtt{C}} -$	
HK2	6a	TCC	
CD 1	7 -	m	
FR1	/a	\mathbf{T}	
VN4	8a	${\tt T}{\tt C}-{\tt NN}{\tt N}{\tt N}{\tt C}{\tt T}{\tt A}-{\tt T}{\tt G}-$	
VN12	۵.5	TATG-	
A 14 T T	Эd	1	
NE98	10a	TT-AA-	



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Fig.1L

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	551	600
HCV-1	15 CCTTGRCTGTCCCGCTTCGGCCTACCAAGTGCGCAA	CTCCACGGGGCTT
HCV-J	1b -TCA-CAC-TG-G	-GTGT-CA-A
HC-G9	1ccACTGT-GG	TTG-G
BNL1	1dG-TAA-KA-CTCG-G	-G-AT-CG-G
BNL2	1dG-TAAA-CTC-TG-G 1fC-CACA-CTTG-GAG	-A-AC-ATGGC
FR2	1fC-CACA-C12	A A C MIGGO
HC-J6	2aA-CCACCG-TCCTGC-GAAG	-ATGTACCGGC
HC-J8	2b C-C A A-TGT AGTGG CA-G	-ATT-GTTCTAGC
S83	2C>-CTA-TCGTGG-GCAAGG-	-AGGC-ACTCC
NE92	2d -TD-CG-TCC-G-TGGCAAG	-AGCA-CTC-
BNL3	26 -TG-CCT-TCT-N-GTTG-GCAAA	TAGTCA-GCC
FR4	2f -TD-CCTGTATAGTAAG	- <u>AA</u> GCC <u>AC'!</u> -C
BNL4	2~ -TC-CCT-TCTGTGGTAAG	-AGTACCA-G
BNL5	25 _TC-CGGC-TGTGGCAAG	-AGCCACTC-
BNL6	2iA-CCG-TCTGTGTGCG	CGGTTTC-
		m> cm m -CC
NZI1	3aA-T-CATAAG-CAGTCTAG-GTGG-	TA-GI-ICC
HCV-TR	3bTGCG-T-G-TAG-GTACACG-	TCTNT-CCC
NE48	3cGTCTGTTAG-A-GGCT-G-GTACG-	-TGTAT-CCC
NE274	3dGTCTGTTG-A-GGATTGTACG 3eCT-TGCTAGTC-GG-TGG-GT	G-AT-CTC
NE145	3eCT-TGCTAGTC-GG-TGG-G-TACA-G3fGT-TCCAGGGCTAG-GTACA-G	A-GT-CCA
NE125		
Z. 4	4aC-CTAGTG-GCTACG	-TG-TTCA-C
Z1 Z1	4bCbbcbbbGTGCTACG-	-TG-TTCG-C
GB358	40CTA-CGT-A-CTAT	-TGTCA-C
DK13	4dCTA-CTAT	AG-T1G-C
GB809	4	-TG-TT
BNL7	AkCCAT-A-CTAT	-TGT-TCA
SNL8	4 LCTTATTA-CTAC	A1CA-C
BNL9	4kCCATTA-CTAC-A	ATCA-C
BNL10	4k -TCCACTA-CTAT	GT-TCA-C
BNL11	4kCCAC-A-CTAC	-TGT-TCA
BNL12	41C	-TGT-TCA
	5a -TCCTGCTAGTT-CCTACA-	-TCT-TA
BE95	5a -100-1G0-1AG11 ccinc n	10 1
нк2	6aC-CAACATCTTACCTACG	A
IIIVZ		
FR1	7aC-CACAACAAATTCAAG-	GT-TA-C
	8aC-TAACAACCGGCGTTATAC	AAGT-TCG
VN4		
VN12	9aC-CCACTCCACTAA-CTATGCT-	AAGT-TG
NE95	10aCT-ACAA-AG-C-GGCTGG-GTACT-	-TGT-CAC
= .		





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Fig.1M

HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	601 1a TACCACGTCACCAATGATTGCCCTAACTCGAGTATTGTGTACGAGGCGGC 1bTGCCTCATA 1cTCCTT-CCCA-CTATA 1dTTCCTT-CCCA-CTATA 1dTTCCTT-CCCA-CTAT-AG 1fTTCTT-CGGCCCA-TAAA
HC-J6 HC-J8 S83 NE92 BNL3 FR4 BNL4 BNL5 BNL5	2aATGGCCA-CTGATCACC-GGC-ACTCCA 2bTCTT-AAACCCACC-GGCCTCA- 2cATGCCGCT-CT-CT-GGCCTT-A 2dATGACAGAGTCCC-GGCCTCAG 2eTATG-CACT-CAACCCA-GGC-ATTN 2fATG-CGTCTG-CTGACCCC-GGCCTCAG 2gATG-CACTT-CAACCCA-C-GGC-AAT-CA 2hTATGGT-AAGCCC-GGCCTTAA 2iATGGT-GAGCCC-GGCCTC-A
NZL1 HCV-TR NE48 NE274 NE145 NE125	3a GT-C-TCCTT-CTAGCTC-A 3b TGTGC-TCCTT-GTGGC
24 21 GB358 DK13 GB809 BNL7 BNL8 BNL9 BNL10 BNL10 BNL11 BNL11	4a -TA
BE95	5aTTT
нк2	6a
FR1	7aTC-T
VN 4	8aTCCCCAGCCCTTA
VN12	9aTTC-ACTAGCCT <u>AA</u>
NE98	10aATGATCCAGGGTCTC-G





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Fig. 1N

HCV-1	651 700 la CGATGCCATCCTGCACACTCCGGGGTGCGTCCCTTGCGTTCGTGAGGGCA
HCV-J	1b GCATGAC-CG-C-CCA-T-
HC-G9	1c GA-CCTGATCTGCTGC-AAC
BNL1	ldG-ATGATACA
BNL2	1d T-C-ATCAT
FR2	ld T-G-ATGTG-CAT-GCAA
1112	lf GCATTGTNGCA-AGA
нс-ј6	2a G-CTGCGTCC
HC-J8	2b T-CAG-TCTCTT-AA-TGAAA-TG-
S83	2c A-GAAG-GTTT-AGT-AGTAGTG
NE 92	2d GTG-TTGTCCT-AGGAGA
BNL3	24 G-G-G-G-T-T-GGC-CT-AGGAGA
FR4	2e GCGG-GTTGTTATCAGAA-AGCTC-G
BNL4	2f G-C-GG-G-C-TGTT-A-TC-T-AGA-GTCA-T-
	2g G-GCGG-GTTGTT-ATGT-AGTTGC
BNL5	2h GTG-G-TGTCT-A-T-T-A-T-AGA-GC-CCAA-
BNL6	2i GGGTGTCTATTCT-AGT-GAA
NZL1	3a TTT
HCV-TR	3b ATGTTTACAGCCACAACC
NE 48	3c -CTTTGCTACC-AAA-CAAT-
NE274	3d TA-TTTGA-T-T-G-CAATCA
NE145	3e ATGTGTTTCG-AGA-C
NE125	3f TATTGCCTGCACT-
24	4a -CCAATTGACTGATGACTG-
21	4b GC-CCAATTGATCTGGACAG-
GB358	4c GC-CCAACTC-ATT-ACGA-G-TTG-
DK13	4d TT-CCAT-ACTCATGA-GAG-
GB809	4e -ACAT-ACTCAACTGAAGACCG-
BNL7	4k -CCATCTCATGA-AG-
BNL8	4k -C-CCATCTA-TGCGA-AACTG-
BNT.9	All CC CA m mcmc
BNL10	4k -CCATTCTCATGCGA-A-TG-
	4k -CCAT-AGCACTATGCGA-A-TG-
BNL11	4k -CCATCTAAGCGAAAA-
BNL12	41 -CCAT-ACTAATACTGAAGACTG-
BE95	5a TA-CCTGAG-ATTGTCATGACAT-
HK2	6a T-C-ATGTTTTGTAT-GT-GA-G-TC-ATG
FR1	7a GACCATGATCTA-TTA-TA-CAAG-CG-
VN4	
· • • •	9a GACACTGTTTTGTTGAAGRT-RA
VN12	9a T-GCATGTCTCTCGAAGACC





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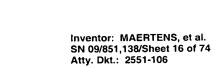
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Fig.10

	_	
HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2 HC-J6	701 1a ACGCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGGCCACCAGGGA 1b -TTTCC-TCAC-CTCCGGA- 1cCT-CC-T-GTCC-TGGTAAA- 1dCATCTCC-CCAC-RC-CC-TGGTAAA- 1dT-TTC-TCAC-RC-CCC-TGGTAA 1f -TATCC-TCACC-CCCC	-C
HC-J8	26 CA CA CA CARACTER	٠.
	2b G-AT-CATCA-ACAAG-AAC-ACTGTG-AAC-	
S83	2cTTC-A	·A
NE92	2dATACC-CA-ACG-TT-GC-ATA-ATGTGCC-	
BNL3	2e GTCGG-TCCACA-CCCT-GC-ACA-AGTGCA-	
FR4	2f -TAGGA-CTTCACAG-CT-GC-ACTGTGCCG	Α
BNL4	2g -TAAGCCCA-ACG-CTC-ACTGTG-ACC-	G
BNL5	2h -TCAGTC-CCA-AC-TGAC-ATGTGCC-	
BNL6	2iACC-CCA-ACG-CACA-CTGTGCC-	
21.20	11 00 0 0 11 110 0 0 1 ACA-C1916C-	. P-
NZL1	3a -TA-AT-CCACCC-AGAAGTT-	·C
HCV-TR	3bCAAATCACACAAG-CT-AA-GGTTAC	Ċ.
NE48	3cAACCA-ACGTGAGGTTC-	
NE274	3dTCAACA-TCGG-AAAGGTT-A-T-	
NE145	3eA-AGACACCCGCAAAGTAT-	
NE125	3f CAGACAC-C-AG-AAGATGTAAC-	
Z4	4aA-AC-TCAC-CGGATGT-GCAC-	·C
Z1	4b -TA-TTC-CCC-CTC-TG-GCCCT-	
GB358	4c -TCAGAC-CCCC-CTCCGG-GCCTT-	
DK13	4dAAGT-CACT-TC-CCCTG-GCAAC-	
GB809	4e CAG C	
BNL7	4k -TCAGAC-TCACC-TCCAG-GCCAT-	_
ENL8	4k -TCAGAC-TCCC-TTCC-AG-GCCAT-	<u></u>
ENL9	4k TCAG-ACT-CC-TIC-AG-GCCAT-	C
BNL10	4k -TCAGTCCC-TCA-CAG-GCCAT-	C
	4k CAGAC-CC	
BNL11	4k -TCATAC-CCCC-TCC-AG-GCCAT-	
BNL12	41A-TC-CCCT-AACG-GCCCAT	A
BE95	5a -T-TGAGTACCCAATACT-AGCC-AG	C
нк2	6a -TCGGC-CCCATTGCCCTACCAA-	-
FR1	7a -T-AGAC-AC-CC-TG-CTC-CT-AGT-CCCA-	С
VN4	8a -TCAACCCCA-GCCTGCCAGTGCC-A-	С
VN12	9aCTGA-C-ACTGCCTGATGGTGCA-A-	-
NE98	10a -TA-AAACA-CC-TGGYCCGTG-A-TC	G





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Fig.1P

HCV-1 HCV-J HC-G9 BNL1 BNL2 FR2	1b 1c 1d 1d	751 GGCAAACTCCCCGCGACGCAGCTTCGACGTCACATCGATCTGCTTGTCGG AGCAA-CACAA-ACGTGCTC-A TCGCGCGTC-GTGGGTGCTC-ACT-GTGA-TRGCAA-CGCTTCT-TGTA-TGGCAA-CC-TGCTG-TCGCGCTATCGATGG-GGGCCCG
HC-J6 HC-J8 S83 NE92 BNL3 FR4 BNL4 BNL5 BNL6	2b 2cd 2e 2f 2p 2h 2i	CC-GGCGC-T-A-CA-GGCT-A-GACGT-CA-GGAT CGGTGCG-T-A-TCGTAGCGACAGCA-A-CAAT CCTGGCGCT-T-A-T-A-GGCGGCAA-CA-CGAT CCTGGTGCG-TTA-C-A-GGCGGACGTTACCA-CA-T-C CCTGGTGCT-T-A-C-A-GGAGGGCA-GTGCCG-CGAT CCTGGTGCT-T-A-T-GAGGTGGGCTACCA-CGAT CCTGGTGCT-T-A-T-GAGGT-GGACGTCACCA-CGAT CC-GGCGC-T-A-C-G-GGTT-GGACGTCACCA-CGAT CCTGGCGCG-T-A-C-G-GGTT-GGACGTCACCA-CTC CCTGGCGCG-TTA-C-A-GGCGGACATTCA-CA
NZL1 HCV-TR NE48 NE274 NE145 NE125	3b 3c 3d 3e	-T-GG-GCAA-TA-TG-TTC-A-ACATG-GCAT-AA CTTGGCG-GAA-CGTC-A-CACCTG-GAGAT-GGTGCGAA-CG-ATC-A-CCG-GGCTGGCGCGAA-TG-ATC-A-CCATG-G
Z4 Z1 GB358 DK13 GB809 BNL7 BNL8 BNL9 BNL10 BNL11	4b 4d 4e 4k 4k 4k 4k	$ \begin{array}{c} {\sf CCGGGCGCTGCTTGA-TC-T-CG-A-TG-GCT-AA-G-ACCA-G-GC-AGCTTAGA-TCCA-GCA-G-TG-ACA-GGACCA-GGACCA-GGACCA-GGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGGACCAGGACCAGGACCAGGACCAGGACCAGGACCAGGACCAGGACCAGGACCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGAGGCCAGGCCAGG$
BE95	5a	CT-GG-GCAGT-AG-T-CTGA-AGC-G-TCTACA-CG
нк2	6a	-CTTCCACGAGGAT-CCA-GTG-GTCG
FR1	7a	TCATC-G-GAATCCACGG-TC-AG-ACCT
VN4	8a	-CGTCTACGA-TCCGG-T-CCAAATG-GCA-CA-GG
VN12	9a	-CGTCGG-GTATC-G-GGTG-CCGAGG-GCCT-GG
NE98	10a	CC-TGCGC-GA-CG-CTCTCCACGG-GA-A-GG





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Fig.1Q

HCV-1	la	801 850 GAGCGCCACCCTCTGTTCGGCCCTCTACGTGGGGGACCTATGCGGGTCTG
HCV-J	1b	-GCGTG-TCTA-GTCAC-
HC-G9	1c	-GCTG-GTTA-GTACCA
BNL1	1d	-G-NNGTCTA-GRT
BNL2	1d	CAG-GT-TCCTA-GCAC-
FR2	1 f	-GCAGTGTCAA-GA-TTTGGC-
		oon 0101 0 1
HC-J6	2a	-TCGCCTTCTGGG-
HC-J8	2h	-GCATGGCCT-GTATG-GG-C-
S83	20	GCA - T - GGC
NE92	24	-TCTTGGTTTTG-GGTCG-GC
	20	ATCTGT-TCTGA-AAGTCG-G-
BNL3	2e	-TCCTGATG-GCG-A-
FR4	21	-TCCG
BNL4	2g	-GTTGTAA-CG-GTCG-G-
BNL5	2h	$-\mathtt{TCT}-\mathtt{T}\mathtt{G}\mathtt{C}-\mathtt{A}-\mathtt{TT}-\mathtt{G}-\mathtt{T}\mathtt{C}\mathtt{T}-\mathtt{C}\mathtt{T}-\mathtt{C}\mathtt{CG}-\mathtt{A}-$
BNL6	2i	-TCGICTT-GI
NZL1	За	CGCGGA-GCTGTTA-GTG
HCV-TR	3b	CGCACGACAAGGGCGCT-TG
NE48	3с	T-CGTAT-GATCTTG-A-
NE274	3d	AGCTTGT-GCCGGTTCTA-GTAG-C-
NE145	3e	C-T-T-T-G-C-C-G-T-T-C-T-T-T-G-C-T-T-T-T-
NE125	3f	TGCAG -GAAT -T -A -TT -GG
Z 4	4 a	CGCGTT-GTTTCAGG
Z 1	4 h	TGCGTTA-GCTA-TA-TGTAGGC-
GB358	4.0	TGCT-TGCGCC-T-TA-CA-CAGGC-
DK13	44	CGTCCA-CAGTGG
GB809	40	mcm
BNI.7	41-	TGCTG-GCCCCGTGGCT
BNL8	4 K	-GCTG-TATA-CTT-RTYGGCT
	4 K	-GCTTG-TC-ATT-GTCGGCT
BNL9	4 K	-GCGTGATT-GTCGG-
BNL10	4 K	AGCTTG-TA-CYT-GTCGGCT
BNL11		-GCTTG-TATA-CTGTGGCT
BNL12	41	TGCATA-CGTTACGG
BE95	5a	AG-G-TGC-C-GT-AAAGCG-TG-AC
HK2	6a	CGCAGTGG-TCATGA-CGTCC
FR1	7a	-GCAGG-AT-TA-GA-CA-CTTAGCA
VN 4	8 a	CGCTG-GTATA-GTGGCC
VN12	9a	TGCTTG-GTCTA-GCTTGGGC
NE98	10a	RGCGACATAATAG-GC





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Fig.1R

		9
	F	351 900
HCV-1	_	TCTTTCTTGTCGGCCAACTGTTCACCTTCTCTCCCAGGCGCCACTGGACG
HCV-J		-TCTCGATC-CGT-TGA
HC-G9		C
BNL1		CC-CTGATAC-CATGCATA
BNL2		C
FR2	lí	CCTGTA-GTCGT
HC-J6	2a	-GA-GCA-CGATTGG-ACAATTT
HC-J8	2b	-GA-GAC-ATCGGGCTTGG-AA-ACAAAACTTC
S83	3.0	-GA-G-G-CCTGG-CGGT-G-GGACAA-ATAC-TTT
NE92		-GA-GT-G-CTTCTG-CT-AGCAATTAA-TTT
BNL3		-GA-GA-A-CT-CAGGCTT-G-GG-AG-AT-ACTTC
FR4		-GA-GA-A-CA-CGG-TGC-GT-GAGCAATATACTTTT
BNL4		-GA-GA-A-CT-CTGG-TGTTGGGCAA-ATAACTTT
BNL5	2h	-GA-GT-GTCTT-TTGACTCAAATCTTC
NZL1	3a	CG-AGCCGAGATC-ATCAA
HCV-TR	3b	-GG-AGCAGATC-CACC
NE48		-TCC-AAGCAA-AC-AAA
NE274		CT-GG-AGGCTAGATC-T-AGAAC
NE145		CGGGCCTAAGGTC-TTTACT
NE125		-TCGCTAGAG-TCAAT-ATC
NEISO	2±	-1C
77 A	4 -	C C C C C D D M MCCC CC M
Z 4		CCGA-GGGAATTCGGGC-TC
Z1	_	CAGGACGAGC-CG
GB358		-AT-GTGAT-TCAGGCT
DK13	4 d	-GCT-GTCAATC-C
GB809	4 e	-ACT-GAA
BNL7	4 k	-GCATGAT-TCGAAT
BNL8		-GCT-GTTGATT-TCGAAC-AT
BNL9		CGCT-GTTGACGAACC
BNL10		-GCT-GTTGATYCAGTCT
BNLll		-GCGTTGAT
BNL12	41	CC-AGGA
BE95	5a	-ACT-GAAATAGGTC-C-AGGCT
HK2	6a	T-G-CGAATCAGC-C-TTT
FR1	7a	-AA-CT-GAGGTTTAGGT-A-TATCA-GTT
- 1.1		
VN4	Q >	-TCCTAGCGCAGGTCATGTCA-GTT
A 7.4 d	54	I C C I A G C GO "NOG"-IO-"NIG-"ICA-GII
tn:10	ο-	CTGGTGAGAATGT-TGATC
VN12	Уa	ATGT-TGATC
0.0		
ИЕ 98	10a	-AT







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Fig.1S

		•
HCV-1 HCV-J		901 950 ACGCAAGGTTGCAATTGCTCTATCTATCCCGGCCATATAACGGGTCACCG GTAAACGT-A
HC-G9 BNL1	1d	AC
BNL2 FR2		AG-AGCA GTG-ACTTCT-TC
HC-J6 HC-J8		$ \begin{array}{cccccccccccccccccccccccccccccccccccc$
S83		GTCG-AACTCACGCTA
NE92 BNL3		GTCG-ACCTCACACTAT GTCG-AA
FR4		GTC-G-AACACACACAAT
BNL4		T-CG-A
BNL5	2h	GTCG-AGA
N2L1	3a	GTCGACCTCGC-GCAC-TT-AAT
HCV-TR		GTGACGCGACAG-TT-AAT
NE48		GTT - GCA C - C A C - G - C - A - T G - TT - A T
NE274		GTGACCAAAAAAAAAAA-
NE145 NE125		GTC-GACCCGT-GCACAAT GTC-GTTGAC-ACAACTA
NEI257	Ji	GIC GIIGA-RC-R-C-R-R-R-R-II-A
Z 4	4 a	G-AGTCCA-TCCA-
21		CG-ACCTTCG-CTCA-
GB358 DK13		G-ACTCCG-GGCG-TCA- CACTCCA-AAAAAAAAAA
GB809		CG-ACTTCCG-AGTCT
BNL7		-TATC
BNL8		G-CG-AT
BNL9		CAC
BNL10 BNL11		CG-ATC CG-AATC
BNL12		GTCACCTC
BULLE	7.1	GIC -ACC-1C
BE95	5a	GTGAACC-TCAGTG-TCC
HK2	6a	GTACCA-ACG-CCA-
FR1	7a	CG-ATCNA-CN-TCG-C <u>A</u> <u>A</u> -
VN4	8a	GTCG-AGTCTCCA-AGCTA
VN12	9a	G-CG-ACCTCG-ACCTG
NE98	10a	GTCG-ACCTC



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Fig.1T

. –3	,	
HCV-1 HCV-J HC-G9 FR2	lb lc	951 957 CATGGCAT AT NNNNNNN
HC-J6 HC-J8 S83 NE92 BNL3 FR4	2b 2c 2d	G T GG G ANN
NZL1 HCV-TR NE48 NE274 NE145 NE125	3c 3d 3e	TG GT GT
Z4 Z1 GB358 DK13 GB809	4b 4c 4d	GG GC GT GT
BE95	5a	G
HK2	6a	GT
FR1	7a	G
VN4	8a	<u>v</u>
VN12	9a	GG



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Fig.2A

HCV1 HCV-J BNL1 BNL2 CAM1078 FR2	la lb ld ld le lf	1 MSTNPKPQKKNKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRR-TXXXXXXX
HCJ6 HCJ8 CH610 NE92 BNL3 FR4	2a 2b 2c 2d 2e 2f	R-T
HCVTR	3b	LRQTLNVV-
DK13 CAM600 GB809 BNL7	4d 4e 4e 4k	R-TM
BE95	5a	R-TM
HK2	6a	LR-TT
FR1	7a	LR-TM
VN4 VN13	8a 8b	LR-TI
VN12	9a	LR-TM
NE98	10a	LR-TXVQV-



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Fig.2B

HCV1 HCV-J	la lb	51 KTSERSQPRGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSP
BNL1 BNL2 CAM1078 FR2	ld ld le lf	X-XSX-XXXXXX
HCJ6 HCJ8 CH610 NE92 BNL3 FR4	2a 2b 2c 2d 2e 2f	
HCVTR	3b	KQ-HLSRSKKL
DK13 CAM600 GB809 BNL7	4d 4e 4e 4k	
BE95	5a	AL
HK2	6a	Q-QH
FR1	7a	V-Q-TS-G
VN4 VN13	8a 8b	V-HQT
VN12	9a	AV-QNQ
NE98	10a	SRTS



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Fig.2C

HCV1 HCV-J	1a 1b	101 RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARA
BNL1 BNL2 FR2	ld ld lf	N NS-T
HC-J6 HC-J8 CH610 NE92 BNL3 FR4	2a 2b 2c 2d 2e 2f	NHVV
HCV-TR	3b	v
GB116 DK13 CAM600 GB809 G22 GB549 GB438 BNL7	4c 4d 4e 4f 4g 4h 4k	VV -XXNX
BE95	5a	NKG-IV
HK2	6a	HNVVVVV
FR1	7a	NNVL-GVL-GV-A-
VN4 VN13	8a 8b	NNXXIE
VN12	9a	D-X-NXV-AE
NE98	10a	N



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Fig.2D

		151
HCV1	la	LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGL
HCV-J	1b	
BNL1	1d	XT-HEAS-V
BNL2	ld	
FR2	1 f	-XXGXXXXXXXXXTE-HST-DG
		_ _
HC-J6	2a	I-T-VAE-K-ISTG
HC-J8	2ъ	
CH610	2c	
NE92	2d	T
BNL3	2 e	XIXXVV-XVE-K-TSQA
FR4	2f	IIV-IK-NSHF
BNL4	2g	VIK-NSHF
BNL5	2ĥ	IVK-TSTM
BNL6	2i	IVK-TSHS
		IIVVA-RS-S
HCV-TR	3b	A-GFFCGLEYT-TS
		TO GETT TS
GB116	4c	-EAVI
DK13	4 cì	-EAVISTVNYAS-V
CAM600	4e	T
GB809	4e	Qv 1
G22	4 £	
GB549		AVI
GB438	4 g	AV
BNL7	4h	Av1
BNL8	4 k	1-F
	4 k	~~_~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
BNL9	4 k	
BNL9	4 k	11XX
BNL10	4 k	~~1~~~~X~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
BNL11	41	IQHYVS-I
	_	
BE95	5a	VPYAS-I
	_	
HK2	ба	AIIT
		111165
FR1	7a	AIIK-AS-I
		1-1-1-K-AS-1
VN4	8a	XXIXXXX-XXXTAHYT-KS
		A A A A A A A A A A A A A A A A A A A
VN12	9a	-XATT
		-XAIIXTLNYA-KS
NE98	10a	·
		I-FFLT-TAGLEYAS



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Fig.2E

HCV-1 HCV-J BNL1 BNL2 FR2	la lb ld ld if	250 YHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRDSM-MS-FLL-A-NSIMDGM-M-YD-HLM-LL-VKXLS-GK-IXIIPLL-A-I
HC-J6 HC-J8 CH610 NE92 BNL3 FR4	2a 2b 2c 2d 2e 2f	-MT-DTWQLQA-VVEKVTIPVS-NVQQ -YAS-NTWQLTVLENDNGTLHIQVNVKH -MSWQLEG-VEQIPVS-NI-Q -MQWQLRVVEKKIIPVS-NI-VSQ -MAS-NWOLXVVENSSGREHIPIS-NI-VSK
BNL4 BNL5 BNL6	2g 2h 2i	-MAA-DWQLRVVE-SRTFT-VS-NVSR -MAS-NIWQMQG-VVELQKIPVNVNQ -MSWQLKVVE-HQ-QIPVNVSQ -MSWQLEE-VVEWKD-TIPVNI-VSQ
HCVTR	3b	-VLS-GE-VLTTQ-STTVSTV-T
GB116 DK13 CAM600 GB809 G22 GB549 GB438 BNL7 BNL8 BNL9 BNL9 BNL9 BNL10 BNL11 GB724	4C 4d 4e 4f 4g 4h 4k 4k 4k 4k 4k	I
BE95	5a	DNLAMTVQILSAPS
HK2	6a	LLDAMLLVDDR-TH-VL-IPN
FR1	7a	LS-NFETMLIKAELPVSL-VPN
VN4	8a	LQASL-VPN
VN12	9a	LNGMLKTLTKLSASL-VQN
NE98	10a	-MS-GG-ILSTIPVSXVKS



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Fig.2F

HCV-1 HCV-J BNL1 BNL2 FR2 HC-J6 HC-J8 CH610 NE92 BNL3 FR4 BNL4 BNL5 BNL6	1a 1b 1d 1f 2a 2b 2c 2d 2e 2f 2p 2h	300 GKLPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWT SSI-T-TIVA-AMSYE- ASV-TXAIVXX-FM-XAM-H- ANV-TAAIVA-VFM-IGTS PGALTQG-TMV-M
HCVTR	3b	LGVTTASI-T-V-MARQAF-AART-
GB116 DK13 CAM600 GB809 G22 GB549 GB438 BNL7 BNL8 BNL9 BNL9 BNL10 BNL11 GB724	4cde4f44k44k44k44k444	VGA-LES-S-V-M-A-VIGM-S-Q LNA-LESV-M-GI-V-GQ AGA-LEPV-M-A-MIGLMQ VGA-LEPV-M-A-V
BE95	. 5a	LGAVTAPAV-Y-A-G-AAALMYRQ-A-
HK2	6a	ASTGFVA-A-VVSILAQ
FR1	7a	SSV-IHGFVA-AFM-IIIR-KY-QV
VN4	8a	AST-V-GF-K-V-IMA-AFMGLLRM-QV
VN12	9a	ASVSIRGV-E-VA-AFMGLRMYEI
NE98	10a	PCAATAST-V-MM-XAALXG-SWRH-Q



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Fig.2G

		301 319
HCV-1 HCV-J	la lb	TQGCNCSIYPGHITGHRMA V-DVS
BNL1	1d	E
BNL2	1d	E
FR2	1f	V-DSXXX
HC-J6	2a	V-D
HC-J8 CH610	2b	EQ
NE92	2c 2d	V-EX V-D
BNL3	2e	V-E
FR4	2f	V-EX
BNL4	2g	S-D
BNL5	2h	V-D
HCVTR	3b	V-TVS
GB116	4c	DAV
DK13	4d	DT
CAM600	4e	DT
GB809 G22	4e 4f	DA
GB549	41 4q	ET DD
GB438	4h	DV
BNL7	4 k	D
BNL8	4 k	A-D
BNL9	4 k	D
BNL9	4 k	D
BNL10 BNL11	4 k	E
GB724	41 4x	V-D DT
	377	D
BE95	5a	V-NSV
HK2	ба	V-DTV
FR1	7a	DXNXV
VN4	8a	V-ET
VN12	9a	A-DA
NE98	10a	V-D



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Fig.3A

SEQ ID NO. 1 (BNL1, 1d)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCTCAKGGSGTN NNNNNNCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGGCCCCAGGNNG GGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCACAACCTCGTGGCAGGCGACAGCCTATCCCCAAGGCTCGYCGGYCCGAGGGCAGGTCCTGGGCTCAGCCCGGGTATCCTTGGCCCTCTATGGCAAT GAGGGCTCCGGGTGGGCGGGTTGCCCCCCGCGGCTCTCGGCCCAATTGGGGCCCC

SEQ ID NO. 3 (BNL1, 1d)

SEQ ID NO. 5 (BNL2, 1d)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCCCCCACAGGACGTC
AAGNTCCCGGGTGGTCGAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGGCCCCAGGTTG
GGTGTGCGCGCGACCAGGAAGACTTCCGAGCGGTCGCAGCCTCGTGACAGGCGACAGCCTATTCCT
AAGGCTCGCCAGTCCGATGGCAGNNCCTGGGCTCAGCCAGGGCATCCCTGGCCCCTCTATGGCAAT
GAGGGCTGCGGATGGGCGGATGGCTCCTGTCCCCCCGCGGCTCTCGGCCCAGTTGGGGCCCC

SEQ ID NO. 7 (BNL2, 1d)

SEQ ID NO. 9 (CAM1078, 1e)



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Fig.3B

SEQ ID NO. 11 (FR2, 1f) ATGAGCACGAATCCTAAAACCTCAAAGAAAAACCAAACGCAACACCGACGCCCCACAGGACGTT AAATTCCCGGGTGGGGGCAGATCGTGGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAGGTTG GGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGCGGAAGGC GACAGCCTATCCCCAAGGCTCGCCGACCCGAGGGCAGGTCCTGGGCTCAGCCTGGGTACC CATGGCCCCTCTATGCTAACGAGGGCTGCGGATGGCGGGATGGCTCCTGTCCCCTCGCG GCTCCCGTCCTAGCTGGGGCCCCAATGACCCCCGACGTAGATCACGCAATTTGGGTAAGG TCATCGATACCCTAACGTGTGGCTTCGCCGATCTCATGGGGTACATTCCGCTCGTCGGCGC CCCCCTAGGGGGCGCTTCCAGAACCCTGNCACATGGTGTCCGGGTCCTGGNAGGCGGCGTGATNNN NNNNNNNNAACCTTCCNGGTTGCTCTTTNNCTATCTTCCTCTTGGCNTTACTCTCTTGCCTCAC AGTCCCCACCTCTGCCTATGAGGTGCACAGCACAACCGATGGCTACCATGTCACTAATGACTGTTC CAACGGCAGCATCGTATATGAGGCAAAGGACATCATCCTTCACACGCCTGGGTGNGTGCCCTGCAT ${ t ACGGGAAGGCAATATCTCCCGTTGCTGGGTACCGCTCACCCCCACGCTCGCAGCGCGGATCGCGAA}$ CGCTCCCATCGATGAGGTGCGGCGTCACGTCGACCTCCTCGTGGGGGGCAGCCGTGTTCTGCTCAGC CATGTACATTGGGGGACCTTTGTGGGGGGGCGTCTTCCTCGTTGGGCAATTGTTCACCTTCACGTCCCG GCGGCATTGGACGGTGCAGGACTGTAATTGTTCCATTTACTCTGGCCACATAACGGGCCACCGNNN

SEQ ID NO. 13 (BNL3, 2e)
ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACCAACCGCCGCCCACAGGACGTC
AAGTTCCCGGGCGGCGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAGATTG
GGTGTGCGCGCGACGAGAAAGACTTCTGAACGGTCCCAGCCACGTGGAAGGCGCCAGCCCATCCCT
AAAGATCGGNGNGCCACTGGCAGGTCCTGGGGAACCTCCAGGATATCCCTGGCCCCTGTATGGGAAC
GAGGGGCTCGGCTGGGCAGGATGCCTCCTGTCCCCCCGAGGCTCTC

SEQ ID NO. 17 (FR4, 2f) ATGAGCACAAATCCTAAACCTCAAAGAAAAACTAAAAGAAACACTAACCGTCGCCCACAGGAC GTTAAGTTCCCGGGCGGCGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAG GTTGGGTGTGCGCGCCCAAGGAAGACTTCTGAACGGTCCCAGCCACGTGGAAGGCGCCAGCCC ATCCCAAAAGATCGGCGCCCCCCTGGCAAGTCCTGGGGACGTCCAGGATACCCTTGGCCCCTGT ACGGGAACGAGGGCTCGGCTGGCCAGGGTGCTCCTCGCCCCCGGGGCTCTCGCCCCTCGTG GGGCCCAAACGACCCCGGCACAGGTCACGCAACTTGGGTAAGGTCATCGATACCCTCACGTG TGGCTTTGSCGACCTCATGGGGTACATACCTGTCGTCGGCGCCCCTGTGGGCGGCGTTGCCAGA GCCCTCGCGCATGGCGTGCGGGTCCTGGAGGACGGGATAAATTATGCAACAGGGAACTTGCCCGGT GTTAAGAACAACAGCCACTTCTACATGGCGACTAATGACTGTGCCAATGACAGCATCGTCTGGCAG CTCAGGGACGCGGTGCTCCATGTTCCTGGATGTGTCCCCTGTGAGAGGTCAGGTAATAGGACCTTC TGTTGGACAGCGGTCTCGCCCAACGTGGCTGTGAGCCGACCTGGTGCTCTCACTAGAGGTCTGCGG GCTCACATTGATACCATCGTGATGTCCGCCACCCTCTGCTCTGCCCTATACATAGGGGACCTATGC GGCGCTGTGATGATAGCAGCGCAAGTTGCCGTCGTCTCACCGCAATACCATACTTTTGTCCAGGAA TGCAACTGCTCCATATACCCAGGCCATATCACAGGACATCGAATGGNN



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Fig.3C

SEQ ID NO. 19 (BNL4, 2g)
GACGGGGTAAATTATGCAACAGGGAATCTGCCTGGTTGCTCTTTCTCTATCTTCTTGTTGGCTCTT
CTGTCTTGTGTCACCGTGCCTGTCTCTGCCGTGCAGGTTAAGAACACCAGTACCATGTACATGGCA
ACCAATGACTGTTCCAACAACAGCATCATCTGGCAAATGCAGGGCGCGGTGCTTCATGTTCCTGGA
TGTGTCCCGTGTGAGTTGCAGGGCAATAAGTCCCGGTGCTGGATACCGGTCACCTCCCAACGTGGCT
GTGAACCAGCCCGGCGCCCTCACTAGGGGCTTGCGGACGCACATTGACACCATCGTGATGGTCGCT
ACGCTCTGTTCTGCACTCTACATCGGGGACGTGTTGTGCGCGCGGTGATGATAGCTGCTCAGGTTGTC
ATTGTCTCGCCGCAACATCACAACTTTTCCCAGGATTGCAATTGTTCCATC

SEQ ID NO. 21 (BNL5, 2h)
ATGAGCACAPATCCTAPACCTCAPAGAPAPACCAPARGAPACACTAPACCGCCGCCCACAGGACGTT
AAGTTCCCGGGCGGTGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGGCCCCCGGTTG
GGTGTGCGCGCGACGAGAPACTTCCGAPCGTCCAGCCACCGTGGGAGGCGCCAGCCCATCCCT
AAAGATCGGCGCTCCACTGGCAPATCCTGGGGACGTCCAGGATACCCTTGGCCCCTGTATGGGAPC
GAGGGCCTTGGTTGGGCAGATGCCTCTTGTCCCCTCGAGGCTCTC

SEQ ID NO. 23 (BNL5, 2h)
GACGGGATAAACTACGCAACAGGGAATCTGCCCGGTTGCTCCTTTTCTATCTTCTTGCTGGCCTTG
CTATCCTGTCTCACTGTGCCGGCGTCCGCTGTGCAGGACACCAGCCACTCTTATATGGTG
ACCAATGATTGCTCAAACAGCAGCATTGTCTGGCAGCTTAAGGATGCTGTGCTTCACGTCCCTGGA
TGTGTTCCATGTGAGAGGCACCAAAATCAGTCTCGCTGCTGGATACCTGTGACACCCAATGTGGCC
GTGAGCCAACCTGGCGCGCTCACCAGGGGTTTGCGGACGCACATTGACACCATCGTTGCGTCTGCT
ACCGTCTGCTCAGCTTTGTATGTGGGCGACTTCTCGCGCGCAGTGATGTTGGTCTCCAATTTTTC
ATGATCTCCCCTCAGCACCACCATCTTCGTCCAGGATTGCAACTGCTCGATA

SEQ ID NO. 27 (BNL7, 4k)
ATGAGCACGAATCCTAAACATCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCCATGGACGTT
AAGTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGGCCCCAGGTTG
GGTGTGCGCGCGACTCGGAAGACTTCGGAGCGGTCGCAACCTCGTGGGAGACGCCAACCTATCCCC
AAGGCGCGTCGATCCGAGGGAAGGTCCTGGGCACACCTAGGCCTCTTTACGGTAAT
GAGGGTTGCGGGTGGGCANNATGGCTCTTGTCCCCCCGCGGTTCTC

SEQ ID NO. 29 (BNL7, 4k)
GACGGGATCAATTTTGCAACAGGGAACCTCCCCGGTTGCTCCTTTTCTATCTTCTCTTTGGCACTC
CTCTCGTGCCTGACTGTCCCCGCTTCGGCCATCAACTATCGCAATGTCTCGGGCATTTACTATGTC
ACCAATGATTGCCCGAATTCAAGCATAGTGTATGAGGCCGACCATCACATCTTGCACCTCCCAGGT
TGCGTGCCCTGCGTGAGAGAGGGGGAATCAGTCACGTTGCTGGGTAGCCCTTACCCCTACCGTCGCA
GCGCCATACATCGGCGCCCACTTGAGTCTCTACGGAGTCATGTGGACTTGATGTGGGGGCCGCC
ACTGTTTGTTCAGCCCTTTACATCGGGGATTTRTGTGGYGGCTTGTTCCTAGTCGGTCAGATGTTC
TCTTTCCGACCAAGGCGCCCACTGGACTACTCAAGATTGCAATTGTTCCATC



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Fig.3D

SEQ ID NO. 35 (BNL10, 4k)
GACGGGATCAATTATGCAACAGGGAATATTCCCGGTTGCTCYTTTTCTATCTTCCTTYTGGCACTT
CTCTCGTGTCTGACTGTCCCCGCTTCGGCCACTAACTATCGCAACGTCTCGGGCATCTACCATGTC
ACCAATGACTGCCCGAATTCAAGCATAGTGTATGAGGCCGACCATCACATCTTAGCACTTCCAGGT
TGCGTGCCCTGCGTGAGAGTGGGGAACCAGTCACGCTGCTGGGTGGCCCTTACCCCTACCGTCGCA
GCGCCATACACCGCGGCGCCGCTTGAGTCCCTGCGGAGTCATGTGGATCTGATGGTGGGAGCTGCC
ACTGTTTGTTCAGCCCTTTACATCGGGGAYTTGTGTGGCGGCTTGTTCTTGGTTGGTCAGATGTTC
TCTTTYCAGCCTCGGCGCCCACTGGACTACCCAGGATTGCAATTGTTCCATC

SEQ ID NO. 45 (VN13, 7a)
ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAACGAAACACCAACCGTCGCCCACAGGACGTC
AAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTCGTTTG
GGTGTGCGCGCGACGAGGAAAACTTCTGAACGGTCCCAGCCCAGGGGTAGACGCCAACCTATACCG
AAGGTGCGTCACCAAACGGGCCGTACCTGGGCTCAACCCGGGTACCCCTGGCCTCTTTATGGGAAT
GAGGGTTGTGGCTGGGCAGGGTGGCTCCTGTCCCCCCNCGGCTCTCGCCCTAATTGGGGCCCTAAT
GACCCCCGGNGGAGGTCCCGCAACCTGGGTAAGGTCATCGATACCCTTACTTGNGGSTTCGCCGAC
CTCATAGAGTACATTCC



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Fig.3E

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SEQ ID NO. 43 (VN4, 7c) ATGAGCACACTTCCAAAACCCCAAAGAAAAACCAAAAGAAACACCATCCGCCGCCCACA GGACGTCAAGTTCCCGGGTGGCGGCCAGATCGTTGGTGGAGTCTACTTGCTGCCGCGCAG GGGCCCGCGCTTGGGTGTGCGCGCGACGAGAAAGACTTCTGAACGGTCCCAGCCCAGAGG TAGGCGCCAACCAATACCCAAAGTGCGCCACCAAACGGGCCGTACCTGGGCCCAGCCCGG CCGCGGCTCTCGCCCAAATTGGGGCCCAAACGACCCCCGGCGAGGTCCCGCAACTTGGG TAAAGTCATCGACACCCTTACTTGCGGCTTCGCCGACCTCATGGGGTATATCCCTGTCGTAG GCGCTCCGWTGGGAGGCGTCGCGGNGGCCTTGGCGCATGGGGTCANGGNCATCGAGGACGGNGTAA ATTACGCAACAGNGAATCTTCCCGGNNGCTCTNTCTCTATCTTNCTCTTGGCACTTCTCTCGTGCC TTACAACACCAGCCTCCGCGGCGCATTATACCAACAAGTCTGGCCTGTACCATCTCACCAACGACT GCCCCAACAGCAGCATCGTTTATGAGGCGGAGACACTGATTTTGCACTTGCCTGGGTGTGTACCTT GTGTGAAGRTGRACAATCAATCCCGGTGCTGGGTGCAGGCCTCCCCGACCCTGGCAGTGCCGAACG CAGCTATGTATGTGGGGGGACCTGTGCGGGGGGCCTTTTCCTCGTTGGACAGCTCTTCACGCTCAGGC CTCGGATGCATCAGGTTGTCCAGGAGTGTAACTGTTCCATCTACACAGGGCATATCACTGGACACC GAATGGCA

SEQ ID NO. 47 (VN12, 7d) ATGAGCACACTTCCAAAACCCCAAAGAAAACCAAAAGAAACACAAACCGTCGCCCAATGGATGTC AAGTTCCCGGGCGGCGGTCAGATCGTTGGTGGAGTCTACTTGTTACCGCGCAGGGGCCCACGTTTG AAGGTGCGCCAGAACCAAGGCCGAACCTGGGCTCAGCCTGGGTACCCCTGGCCCCTTTATGGGAAC GAGGGCTGCGGCTGGGCGGGTGGCTCTTGTCCCCCCGTGGCTCTCGCCCGGACTGGGGNCCCAAT GACCCCGGNGGAGGTCCCGCAACCTGGGTAAGGTCATCG ACACCCTCACTTGCGGCTTCGCCGACCTCATGGAGTACATCCCTGTCGTTGGCGCCCCCCT TGGAGGCGTTGCGGCGGAACTGGNACATGGTGTCAGGGCCATCGAGGACGGGATAAACTATGCAAC AGGGAATCTTCCTGGTTGCTCTTTCTCTATCTTCCWCTTGGCACTTCTCTCGTGCCTCACCACGCC TGCCTCCGCACTAAACTATGCTAACAAGTCTGGGCTGTATCATCTAACCAATGACTGCCCCAATAG CAGCATTGTGTATGAGGCGAATGGCATGATCCTGCATCTCCCGGGTTGCGTCCCCTGCGTGAAGAC CGGCAACCTGACCAAGTGTTGGCTGTCGGCCTCCCCGACATTGGCGGTGCAGAATGCGTCGGTGTC ${\tt CGTGGGCGACTTATGCGGTGGGCTCTTTCTCGTTGGGCAGTTGTTCACGTTCAGACCCAGGATGTA}$ TGAGATCGCCCAGGACTGCAACTGTTCCATCTATGCAGGCCACATCACTGGGCACCGGATGGCG

SEQ ID NO. 41 (FR1, 9a) ATGAGCACACTTCCAAAACCCCAAAGAAAACCAAAAGAAATACTAACCGTCGCCCTATGGAC GTCAAGTTCCCGGGCGGCGGCCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGC CCTCGTTTGGGTGTGCGCGCGACGAGAAAGACCTCCGAACGGTCCCAGCCTAGAGGCAGG CGCCAGCCCATACCAAAGGTACGCCAGCCGACAGGCCGTAGCTGGGGTCAACCCGGCTAC CCTTGGCCCCTTTATGGCAACGAGGGCTGCGGATGGCGGGATGGCTCCTGTCCCCCGC GGGTCTCGTCCTAATTGGGGCCCCAACGACCCCCGGCGAAGGTCCCGCAACTTGGGTAAG GTCATCGATACCCTTACATNCGGNCTAGCCGACCTCATGGGGTACATCCCTGTCCTAGGAGG GCCGCTTGGCGGCTTGCCGCTGGCGCATGGCGTTAGGGCAATCGAGGACGGGGTCAATTA CGCAACAGGGAATCTTCCTGGTTGCTCCTTTTCTATCTTCCTCTTAGCACTGTTATCGTGCCTCAC TACACCAGCCTCAGCAATTCAAGTCAAGAACGCCTCTGGGATCTACCATCTTACCAATGACTGCTC GAACAACAGCATCGTTTTTGAGGCGGAGACCATGATACTGCATCTTCCAGGTTGTGTCCCATGTAT CAAGGCGGGGAATGAGTCACGATGTTGGCTCCCTGTCTCCCCCACCTTAGCCGTCCCCAACTCATC AGTGCCAATCCACGGGTTTCGCCGACACGTAGACCTCCTCGTTGGGGCAGCGGCATTTTGTTCGGC CATGTACATCGGAGACCTCTGTGGTAGCATAATCTTGGTAGGCCAGCTTTTTACTTTCAGGCCTAA GTACCATCAGGTTACCCAGGATTGTAACTGCTCTATNAACNCTGGCCACGTCACGGGACACAGGAT **GGCA**



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Fig.3F

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SEQ ID NO. 49 (NE98, 10a)

ATGAGCACACTTCCTAAACCACAAGAAAAACCAAAAGAAACACCAACC?CCGGCCACAGGACGTT
AAGTTCCCAGGCGGCGGTCAGATCGTTGGTGGAGTTTACGTGCTACCACGCAGGGGCCCCCAGTTG
GGTGTGCGTGCAGTGCGCAAGACTTCCGAGCGGTCGCAACCTCGCAGTAGGCGCCAACCCATCCCC
AGGGCGCGCCGAACCGAGGGCAGGTCCTGGGCTCAGCCCGGGTACCCTTGGCCCCTATATGGGAAT
GAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCGCGCGCTCTC

SEQ ID NO. 51 (NE98, 10a)

SEQ ID NO. 53 (BNL1,1d)

CTCGACAGTTACTGAGAATGACATCCGTGTCGAGGAATCAATATACCAATGTTGTGACTTGGCCCCCGAGGCTCGCAAGGCCATAAAGTCGCTCACCGAGCGGCTGTACATCCGGGGGCCCYCTAACCAATTCAAAAGGACAGAACTGCGGCTACCGTCGGTGCCGCGCCAGCGGCGTGCTGACTACCAGCTGCGGCAACCCCTGACATGCTACTTGAAAGCCAGAGCGGCCTGTCGAGCTGCAAAGCTCCGGGACTGCACCATGCTCGTGTGCGGGAATGACCTTGTCGTTATCTGTGAGAGTGCGGGAGTCGAGGAAGACGCGGCGAACCCTACGAGCT

SEQ ID NO. 55 (BNL2,1d)

CTCGACAGTTACTGAGAACGACATCCGTACCGAGGRATCAATCTATCAATGTTGTGACTTGGCCCC
YGAGGCCCGCAAGGCCATAAAGTCGCTCACCGAGCGGCTGTACGTCGGGGGCCCCCTAACCAATTC
AAAGGGGCAGAACTGCGGCTATCGTCGGTGTCGCGCTAGCGGCGTGCTGACCACCAGCTGCGGCAA
CACCCTCACATGCTACTTGAAAGCCAGGGCGGCCTGTCGAGCTGCAAAGCTCCAGGACTGCACGAT
GCTCGTGTGCGGAGACGACCTTGTCGTTATCTGTGAGAGCGCGGGAGTCGAGGAGGACGCGGGGAA
CCTACGAGTC

SEQ ID NO. 57 (FR17,1d)

SEQ ID NO. 59 (CAM1078,1e)

CGTACAGCCTCCAGGACCCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAG
TACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGA
GATTTGGGCGTGCCCCCGCAAGACTGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTG
TGGTACTGCTGATAGGGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCAT
GAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCCACAGGA
CGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGCTCTACCGCGCAGCGG
CCCTAGATTGGGTGTGCGCGCAGCGCGGAAGACTTCGGAGCGGTCGCAACCTCGTGGGAG
GCGCCAACCTATTCCCAAGGAGCGCCGACCCGAGGTCCTGGGCGCAGCCCGGGTA
CCCCTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCCAGGTCCTGTCCCCTCG
CGGCTCCCGTCCTAGTTGGGGTCCTACTGACCCCCGGCGTAGGTCACCCAATTTGGGTAA
GGTCATCGATACCCTCACGTGTTGNTTCGCCGACCTCATGGGGTACATACCG



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Fig.3G

SEQ ID NO. 61 (CAM1078, le)

CTCAACGGTCACTGAAGCTGATATCCGAACAGAGGAGTCCATATACCAATGCTGTGACCTGCACCC
CGAAGCACGTGTAGCCATCAAGTCTTTGACTGAAAGGCTGTACGTCGGGGGGCCCTTGACCAATTC
AAAAGGGGAGAACTGCGGCTATCGCAGATGCCGTGCCAGCGGCGTCTTGACAACCAGCTGCGGCAA
CACCCTCACCTGCTATATCAAGGCCCTAGCAGCCTGTAGAGCTGCCAAGCTCCAGGACTGCACCAT
GCTCGTCTGTGGCGACGACCTGGTCGTGATCTGCGAGAGTGTAGGGACCCAGGAGGATGCGGCGAG
CCTGCGAGCC

SEQ ID NO. 63 (FR2, 1f)

SEQ ID NO. 65 (FR16, 1g)

SEQ ID NO. 67 (FR16,1q)

SEQ ID NO. 69 (BNL3, 2e)

CTCGACAGTCACAGAGAGAGATATAAGNACTGAGGAGTCCATATACCAGGCTTGTTCCTTACCCGA GCAGGCCAGAACTGCCATACACTCATTGACTGAGAGACTCTACGTAGGAGGGCCCATGATGAACAG CAAAGGGCAATCCTGCGGATACAGGCATTGCCGCGCCAGCGGAGTGCTCACCACCAGTATGGGGAA TACCATCACGTGCTACATCAAGGCCCTAGCGGCTTGTAAAGCAGCAGGAATAGTGGCCCCCACCAT GCTGGTGTGCGGCGATGACCTAGTTGTCATCTCAGAGAGTCAGGGAGTCGAGGAGGACGACCGGAA CCTGANNNNN



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Fig.3H

SEQ ID NO. 71 (FR4, 2f)

CTCAACCGTCACAGAGAGGGATATAAGAACTGAGGAGTCCATATACCTGGCCTGCTCCTTACCCGA GCAGGCCCGGACTGCCATACATTCATTAACTGAGAGACTTTACGTGGGAGGGCCCATGATGAACAG CAAAGGGCAGTCCTGCGGATACAGGCGTTGCCGCGCTAGCGGAGTGCTCACCACCAGTATGGGGAA CACCATCACGTGTTATGTGAAAGCCCTCGCAGCTTGTAAAGCTGCGGGCCATTGTTGCCCCCACGAT GCTGGTGTGCGGCGATGACCTGGTTGTCATCTCAGAGAGTCAGGGGGCTGAGGAGGACGAGCGAAA CCTGAGAGTC

SEO ID NO. 73 (BNL5,2h)

CTCAACAGTCGCGGAGAGAGACATCAGGACCGAGGAGTCCATTTACCTTGCCTGCTCCTTACCCGA GCAAGCCCGAACTGCCATACATTCATTGACTGAGAGACTTTACGTAGGAGGGCCCATGATGAACAG CAAGGGACAGTCCTGCGGTTACAGACGTTGCCGCGCCAGCGGAGTGCTCACCACCAGCATGGGGAA TACCATCACATGCTATGTGAAGGCATTAGCTGCCTGCAAAGCTGCAGGCATCGTTGCTCCCACGAT GCTGGTTTGTGGCGACGATCTGGTCATCATCTCAGAGAGTCAGGGAACCGAGGAGGATGAGCGGAA CCTGAGAGTC

SEQ ID NO. 75 (FR13, 2k)

CGNACANCCTCCAGGCCCCCCCCCCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAG TACACCGGAATTGCCGGGAAGACTGGGTCCTTTCTTGGATAAACCCACTCTATGCCCGGC CATTTGGGCGTGCCCCGCAAGACTGCTARCCGAGTAGCGTTGGGTTGCGAAAGGCCTTG TGGTACTGCCTGATAGGGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCATCAT GAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACTAACCGCCGCCCACAGGA CGTTAAGTTCCCGGCGGTGGCCAGATCGTTGGCGGAGTATACTTGTTGCCNTGCAGGGG NCCCAGGTNGNGTNTATGCGCAACGANGAAGACTNCCGAACAGTCCCAGCCACGTGGGAG GCGCCAGCCCATCCCGAAAGATCGGNGCACCACTGGCAAGTCCTGGGGACGTCCAGGATA TCCCTGGCCCCTGTATGGGAACGAGGGCCTCGGGTGGGCAGGGTGGCTCCTGTCCCCCG GGGCTCCCGCCCGTCATGGGGCCCCACGGACCCCCGGCATAGGTCGCGCAACTTGGGTAA GGTCATCGATACCCTCACGTNCGGCTTTNCCGACCTCATGGGGTACATTCCCGTCGTTGG CGCCCAGTAGGNGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGG TCTGTCCTGAATTACCGNGCCAGTTTCTGCTGTGGAAATCAAAAACACCAGMAACACATA CATGGTGACTAACGACTGTTCAAACAGYAGCATCACCTGGCAGCTTNNGNNCGCGGTGCT TCACGTTCCTGGATGCGTCCCCTGTGAACGAGGGCCAACAGTTCCCGGTGCTGGATTCC AGTCACGCCCRACGTAKNCGTGAGCCGACCTGGTGCCCTAACCGAGGGTTTGCGATCGCA CATCGACACCATCGTAGCGTCCGCAACATTTTGTTCTGCCCTCTACATAGGGGATGTATG TGGCGCGATAATGATAGCTGCCCAAGTGGTCATCGTCTCGCCGGAGCATCATCACTTTGT CCAGGACTGTAACTGTTCCATCTACCCGGGCCACATAACGGGGCCTCGTATGTNG

SEQ ID NO. 77 (FR13, 2k)

ATCCACAGTCACTGAAAGAGACATCAGAGTTGAAGAGTCCGTTTATCTGTCCTGTTCACTTCCCGA GGAGGCCCGAGCTGCCATACACTCACTAACTGAGAGGCTGTACGTGGGAGGTCCCATGCAGAACAG CAAGGGGCAATCCTGCGGATACAGGCGCTGCCGCGCCAGCGGGGTGCTCACCACTAGCATGGGGAA TACTCTCACATGCTACTTGAAGGCCCAGGGGGCCTGCAGGGCCGGGGCATTGTTGCACCCACAAT GCTGGTGTGTGGCGACGACCTGGTCGTCATCTCAGAGAGTCAGGGGACTGAGAGGGACGAGAACAA CCTGAGACCT



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Fig.3I

SEQ ID NO. 79 (FR18,21)

CTCAACAGTCACGGAGAGGGACATCAGGAATGAGGAGTCCATATTCCTGGCCTGCTCGTTGCCCGA GGAGGCCCGGACTGTCATACATTCGCTCACTGAGAGACTCTACATAGGCGGGCCGATGATGAACAG CAAAGGCCAGTCCTGTGGATACAGGCGTTGTCGCGCCAGCGGGGTGTTCACCACTAGCATGGGCAA TACCATCACGTGCTATGTGAAAGCCATGGCAGCTTGCAGAGCTGCCGGGATTGACGCCCCCACAAT GTTGGTATGTGGCGACGACCTGGTGGTCATCTCAGAGAGTCAGGGGACCGAGGAGGACGAAA TCTGAGAGTC

SEO ID NO. 81 (PAK64,3q)

CTCTTGACTCTACTGTCACTGAACAGGATATCAGGGTAGAAGAAGAATATACCAATGTTGTGACC
TTGAGCCGGAGGCTAGACGGGCAATCAAATCGCTCACGGAACGGCTTTACGTTGGAGGTCCCATGT
TCAACAGCAAGGGGCTCAAATGCGGATATCGCCGTTGCCGTGCTAGCGGTGTATTGCCCACTAGCT
ACGGTAATACAATCACCTGCTACATCAAGGCCAGAGCGGCTGCTCGAGCTGCGGGCCTTCAAGACC
CATCATTCCTTGTCTGCGGAGATGATTTGGTGGTAGTGGCTGAGAGTTGCGKCGTTGATGAGGAGG
ATAGGGCAGC

SEQ ID NO. 83 (BNL8, 4k)

SEQ ID NO. 85 (BNL12,41)

CTCCACGGTGACTGAAAAGGACATCAGGGTCGAGGAAGAGATCTATCAATGTTGTGACCTGGARCC CGAAGCCCGCAAAGCAATATCCGCCCTCACAGAGAGAGACTCTACTTGGGCGGCCCCATGTATAACAG CAAAGGGGAGCTCTGCGGGTATCGGAGGTGCCGCGAGCGGAGTGTACACCACAAGTTTCGGGAA CACAGTGACCTGCTATCTTAAGGCCACCGCAGCTACCAGGGCTGCAGGCCTAAAAGACTGCACCAT GCTGGTCTGCGGTGACGACTTCGTCGTCATCGCCGAGAGCGAGGGCGTAGAGGAGGATTCCCAACC CCTCCGAGCC

SEQ ID NO. 87 (EG61, 4m)

SEQ ID NO. 89 (VN13,7a)

CTCAACAGTCACAGAGCGCGATGTCCAGACGGAGCATGACATCTACCAGTGCTGTAAGTTGGAGCC CGCAGCACGGACAGCCATCACATCGCTTACTGACCGATTGTACTNCGGTGGTCCCATGTNTAACTC TAAAGGTCAGGCATGTGGATACCGTAGGTGCAGGGCCAGTGGCGTCTTGACCACCATCCTGGCCAA TACTCTGACTTGCTACTTGAAAGCTCAGGCGGCATGCAGAGCTGCCGGGCTGAAGGACTTTGACAT GTTGGTCTGCGGAGACGACCTTGTCGTTATTTCGGAGAGTTTGGGGGTCTCGGAGGACACTAGTGC ACTGCGAGCT



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Fig.3J

SEQ ID NO. 91 (VN4,7c)

SEQ ID NO. 93 (VN12,7d)

SEQ ID NO. 95 (FR1, 9a)

SEQ ID NO. 97 (NE98, 10a)

SEQ ID NO. 99 (FR14,11a)

SEQ ID NO. 101 (FR15, 11a)





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Fig.3K

SEQ ID NO. 103 (FR19,11a)

CGTACAGCCTCCAGGACCCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACC
GGAATTGCCGGGAAGACTGGGTCCTTTCTTGGATTAACCCACTCTATGCCCGGAGATTTGGGCGTG
CCCCCGCAAGACTGCTAGCCGAGTAGCGTTGGGTTGCGAAAGGCCTTGTGGTACTGCCTGATAGGG
TGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACCTCAAAG
ACAAACCAAAAGAAACACCAACCGCCGCCCACAGGACGTTAAGTTCCCGGGCGGTGGCCAGATCGT
TGGCGGGGTGTACTTGTTGCCGCGCAGGGGCCCCAACCTATCCCCAAGGTTAGGCGCACCACCGGCCGTT
GGAGCGGTCCCAGCCGCGCGGGAGGGCCCCAACCTATCCCCAAGGTTAGGCGCACCACCGGCCGTT

SEQ ID NO. 105 (FR19,11a)

CTCTACTGTCACAGAGAGGGATATACGAACAGAGGAATCCATYTATCTGGCTTGTCAATTGCCCGA AGAGGCCCGGAAGGCCATCAAATCACTGACAGAGAGACTATACGTGGGCGGCCCGATGGAAAACAG CAAGGGCCAGGCCTGCGGATACAGGCGTTGCCGCGCAAGCGGGGTATTCACCACAAGCTTGGGGAA CACCATGACTTGTTACATCAAAGCCAAGGCGGCTTGTAAAGCCGCTGGCATTGTTGACCCAGTGAT GCTCGTGTGCGGCGACGACCTAGTGGTCATCTCAGAAAGCAAGGGGGTGGAGGAGGACCAACGAGA CCTACGANTC

SEQ ID NC. 2 (BNL1, 1d)

MSTNPKPQRKTKRNTNRRPXXXXXPGGGQIVGGVYLLPRRGPRXGVRATRKTSERSQPRGRRQPIP KAXRXEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPNWGP

SEQ ID NO. 4 (BNL1, 1d)

DGVNYATGNLPGCSFSIFLLALLSCLTVPXTAHEVRNASGVYHVTNDCSNSSIIYEMDGMIMHYPGCVPCVREDNHLRCWMALTPTLAVKXASVPTXAIRRHVDLLVGXXTFCSAMYVXDLCGSVFLAGQLFTFSPRMHHTTQECNCSI

SEO ID NO. 6 (BNL2, 1d)

MSTNPKPQRKTKRNTNRRPQDVKXPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRDRRQPIP KARQSDGXXWAQPGHPWPLYGNEGCGWAGWLLSPRGSRPSWGP

SEQ ID NO. 8 (BNL2, 1d)

DGVNYATGNLPGCSFSIFLLAFLSCLTVPTTAHEVRNASGVYHLTNDCSNSSIIYEMSGMILHAPG CVPCVRENNSSRCWMXLTPTLAVKDANVPTAAIRRHVDLLVGTAAFRSAMYVGDLCGSVFLVGQLF TFSPRLYHTTOECNCSI

SEQ ID NO. 10 (CAM1078, le)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRAARKTSERSQPRGRRQPIP KERRPEGR

SEQ ID NO. 12 (FR2, 1f)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KARRPEGRSWAQPGYPWPLYANEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKVIDTLTCGFAD LMGYIPLVGAPLGGASRTLXHGVRVLXGGVXXXXXNLXGCSXXIFLLXLLSCLTVPTSAYEVHSTT DGYHVTNDCSNGSIVYEAKDIILHTPGXVPCIREGNISRCWVPLTPTLAARIANAPIDEVRRHVDL LVGAAVFCSAMYIGDLCGGVFLVGQLFTFTSRRHWT VODCNCSIYSGHITGHXXX

SEQ ID NO. 14 (BNL3, 2e)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KDRXATGRSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWG

SEQ ID NO. 16 (BNL3, 2e)

TCXXADLMGYXPVVGAPVGGXARALAXGVRVLEDGINYXTGNLPGCSFSIFXLALLSCVTVPVSXV EVKNTSQAYMATNDCSNNSIVWQLXDAVLHVPGCVPCENSSGRFHCWIPISPNIAVSKPGALTKGL RARIDAVVMSATLCSALYVGDVCGAVMIAAOAFIVAPKRHYFVOECNCSIYPGHITGHRMA



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Fig.3L

SEQ ID NO. 18 (FR4, 2f)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRAPRKTSERSQPRGRRQPIP
KDRRATGKSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNLGKVIDTLTCGFXD
LMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLSCITVPVSAIQVKNNS
HFYMATNDCANDSIVWQLRDAVLHVPGCVPCERSGNRTFCWTAVSPNVAVSRPGALTRGLRAHIDT
IVMSATLCSALYIGDLCGAVMIAAQVAVVSPQYHTFVQECNCSIYPGHITGHRMX

SEQ ID NO. 20 (BNL4, 2g)
DGVNYATGNLPGCSFSIFLLALLSCVTVPVSAVQVKNTSTMYMATNDCSNNSIIWQMQGAVLHVPG
CVPCELQGNKSRCWIPVTPNVAVNQPGALTRGLRTHIDTIVMVATLCSALYIGDVCGAVMIAAQVV
IVSPQHHNFSQDCNCSI

SEQ ID NO. 22 (BNL5, 2h)
MSTNPKPQRKTKRNTNRRPQDVKFPGGGRSLAEYTCARRGKLRRSSMG

SEQ ID NO. 24 (BNL5, 2h)
DGINYATGNLPGCSFSIFLLALLSCLTVPASAVQVKNTSHSYMVTNDCSNSSIVWQLKDAVLHVPG
CVPCERHQNQSRCWIPVTPNVAVSQPGALTRGLRTHIDTIVASATVCSALYVGDFCGAVMLVSQFF
MISPOHHIFVODCNCSI

SEQ ID NO. 26 (BNL6, 2i)
DGINYATGNLPGCSFSIFLLALLSCITVPVSAVQVANRSGSYMVTNDCSNSSIVWQLEEAVLHVPG
CVPCEWKDNTSRCWIPVTPNIAVSQPGAXTKGLRTHIDIIVASATFCSALYV

SEQ ID NO. 28 (BNL7, 4k)
MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP
KARRSEGRSWAQPGYPWPLYGNEGCGWAXWLLSPRGSRPSWGPNDPRRRSR

SEQ ID NO. 30 (BNL7, 4k)
DGINFATGNLPGCSFSIFLLALLSCLTVPASAINYRNVSGIYYVTNDCPNSSIVYEADHHILHLPG
CVPCVREGNQSRCWVALTPTVAAPYIGAPLESLRSHVDLMVGAATVCSALYIGDXCXGLFLVGQMF
SFRPRRHWTTQDCNCSI

SEQ ID NO. 32 (BNL8, 4k)
DGINYATGNLPGCSFSIFLLALLSCLTVPASAINYRNTSGIYHVTNDCPNSSIVYEADHHILHLPG
CVPCVRTGNQSRCWVALTPTVAAPYIGAPLESLRSHVDLMVGAATVCSALYIGDLCGGLFLVGQMF
SFRPRRHWTAODCNCSI

SEQ ID NO. 34 (BNL9, 4k)
DGINYATGNLPGCSFSIFLLALLSCLTVPASAINYHNTSGIYHITNDCPNSSIVYEADHHILHLPG
CVPCVRVGNQSSCWVALTPTIAAPYIGAPLESIRSHVDLMVGAATVCSALYIGDLCGGAFLVGQMF
SFRPRRHWTTQDCNCSI

SEQ ID NO. 36 (BNL10, 4k)
DGINYATGNIPGCXFSIFLXALLSCLTVPASATNYRNVSGIYHVTNDCPNSSIVYEADHHILALPG
CVPCVRVGNQSRCWVALTPTVAAPYTAAPLESLRSHVDLMVGAATVCSALYIGXLCGGLFLVGQMF
SXQPRRHWTTQDCNCSI

SEQ ID NO. 38 (BNL11, 4k)
DGINYATGXLPGCSFSIFLLALLSCLTVPASATNYRNVSGIYHVTNDCPNSSIVFEADHHILHLPG
CVPCVKEGNHSRCWVALTPTVAAPYIGAPLESLRSHVDVMVGAATVCSALYIGDLCGGLFLVGQMF
SFRPRHWTTQECNCSI

SEQ ID NO. 40 (BNL12, 41)
DGINYATGNLPGCSFSIFILALLSCLTVPASAQHYRNVSGIYHVTNDCPNSSIVYESDHHILHLPG
CVPCVKTGNTSRCWVALTPTVAAPILSAPLMSVRRHVDLMVGAATLSSALYVGDLCGGAFLVGQMF
TFQPRRHWTVQDCNCSI



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Fig.3M

SEQ ID NO. 46 (VN13, 7a)

MSTLPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KVRHQTGRTWAQPGYPWPLYGNEGCGWAGWLLSPXGSRPNWGPNDPRXRSRNLGKVIDTLTXXFAD LIEYI

SEQ ID NO. 44 (VN4, 7c)

MSTLPKPQRKTKRNTIRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KVRHQTGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLGKVIDTLTCGFAD LMGYIPVVGAPXGGVAXALAHGVXXIEDXVNYATXNLPXXSXSIXLLALLSCLTTPASAAHYTNKS GLYHLTNDCPNSSIVYEAETLILHLPGCVPCVKXXNQSRCWVQASPTLAVPNASTPVTGFRKHVDI MVGAAAFCSAMYVGDLCGGLFLVGQLFTLRPRMHQVVQECNCSIYTGHITGHRMA

SEQ ID NO. 48 (VN12, 7d)

MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQARGRRQPIP KVRQNQGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPDWXPNDPRXRSRNLGKVIDTLTCGFAD LMEYIPVVGAPLGGVAAELXHGVRAIEDGINYATGNLPGCSFSIFXLALLSCLTTPASALNYANKS GLYHLTNDCPNSSIVYEANGMILHLPGCVPCVKTGNLTKCWLSASPTLAVQNASVSIRGVREHVDL LVGAAAFCSAMYVGDLCGGLFLVGQLFTFRPRMYEIAQDCNCSIYAGHITGHRMA

SEQ ID NO. 42 (FR1, 9a)

MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKVRQPTGRSWGQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRSRNLGKVIDTLTXXLADLMGYIPVLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLALLSCLTTPASAIQVKNASGIYHLTNDCSNNSIVFEAETMILHLPGCVPCIKAGNESRCWLPVSPTLAVPNSSVPIHGFRRHVDLLVGAAAFCSAMYIGDLCGSIILVGQLFTFRPKYHQVTQDCNCSXNXGHVTGHRMA

SEQ ID NO. 50 (NE98, 10a)

MSTLPKPQRKTKRNTNXRPQDVKFPGGGQIVGGVYVLPRRGPQLGVRAVRKTSERSQPRSRRQPIPRARRTEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRR

SEQ ID NO. 52 (NE98, 10a)

DGINFATGNLPGCSFSIFLLALFSCLLTPTAGLEYRNASGLYMVTNDCSNGSIVYEAGDIILHLPGCVPCVRSGNTSRCWIPVSXTVAVKSPCAATASLRTHVDMMVXAATLCSALYVGDLCGALFLXGQGFSWRHRQHWTVQDCNCSI

SEQ ID NO. 54 (BNL1,1d)

STVTENDIRVEESIYQCCDLAPEARKAIKSLTERLYIGGXLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARAACRAAKLRDCTMLVCGDDLVVICESAGVEEDAANLRA

SEQ ID NO. 56 (BNL2,1d)

STVTENDIRTEXSIYQCCDLAXEARKAIKSLTERLYVGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARAACRAAKLQDCTMLVCGDDLVVICESAGVEEDAANLRV

SEQ ID NO. 58 (FR17,1d)

STVTENDIRVEESIYQCCDLAPEARKAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKARAACRAAKLQDCTMLVCGDDLVVICESMGVEEDAANLRV



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Fig.3N

SEQ ID NO. 60 (CAM1078, le)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRAARKTSERSQPRGRRQPIP KERRPEGRSWAQPGYPWPLYGNEGCGWAGXLLSPRGSRPSWGPTDPRRRSRNLGKVIDTLTCXFAD LMGYIP

SEQ ID NO. 62 (CAM1078, le)

STVTEADIRTEESIYQCCDLHPEARVAIKSLTERLYVGGPLTNSKGENCGYRRCRASGVLTTSCGN TLTCYIKALAACRAAKLQDCTMLVCGDDLVVICESVGTQEDAASLRA

SEQ ID NO. 64 (FR2, 1f)

STVTESDIRTEESIYQCCDLDPEARKAIRSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYIKARAACRAAKLQDCSMLVCGDDLVVICEIEGXXEDPSXXXX

SEQ ID NO. 66 (FR16, 1g)

MSTNPKPQRKTKRNINRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIP KARRSEGRSWAQPGYPWPLYGNEGMGWAGWLLSPHGSRPSWGPSDPRRRSRNLGKVIDTLTCGFAD LMGYIPLVGAPLGGVARALAQGFRDL

SEQ ID NO. 68 (FR16, 1q)

XXVTESDIRVEXSIYQCCDLAPEARVAIKSLTERLYVGGPLTNSKGQNCGYRRCRASGVLTTSCGN TLTCYLKAAAACRAAKLRECTMLVCGDDLVVICESAGVQEDAASXXX

SEQ ID NO. 70 (BNL3, 2e)

STVTERDIXTEESIYQACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRHCRASGVLTTSMGN TITCYIKALAACKAAGIVAPTMLVCGDDLVVISESQGVEEDDRNLXX

SEQ ID NO. 72 (FR4, 2f)

STVTERDIRTEESIYLACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRRCRASGVLTTSMGN TITCYVKALAACKAAGIVAPTMLVCGDDLVVISESQGAEEDERNLRV

SEQ ID NO. 74 (BNL5, 2h)

STVAERDIRTEESIYLACSLPEQARTAIHSLTERLYVGGPMMNSKGQSCGYRRCRASGVLTTSMGN TITCYVKALAACKAAGIVAPTMLVCGDDLVIISESQGTEEDERNLRV

SEQ ID NO. 76 (FR13,2k)

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLXCRXPRXXXCATXKTXEQSQPRGRRQPIP KDRXTTGKSWGRPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHRSRNLGKVIDTLTXGFXD LMGYIPVVGAPVXGVARALAHGVRVLEDGINYETGNLPGCSFSISLLALLSITXPVSAVEIKNTXN TYMVTNDCSNXSITWQLXXAVLHVPGCVPCEREGNSSRCWIPVTPXVXVSRPGALTEGLRSHIDTI VASATFCSALYIGDVCGAIMIAAQVVIVSPEHHHFVQDCNCSIYPGHITGPRMX

SEQ ID NO. 78 (FR13, 2k)

STVTERDIRVEESVYLSCSLPEEARAAIHSLTERLYVGGPMQNSKGQSCGYRRCRASGVLTTSMGN TLTCYLKAQAACRAAGIVAPTMLVCGDDLVVISESQGTERDENNLRP



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Fig.30

SEQ ID NO. 80 (FR18,21)

STVTERDIRNEESIFLACSLPEEARTVIHSLTERLYIGGPMMNSKGQSCGYRRCRASGVFTTSMGN TITCYVKAMAACRAAGIDAPTMLVCGDDLVVISESQGTEEDFRNLRV

SEQ ID NO. 82 (PAK64, 3q)

STVTEQDIRVEEEIYQCCDLEPEARRAIKSLTERLYVGG2MFNSKGLKCGYRRCRASGVLPTSYGN TITCYIKARAARAAGLQDPSFLVCGDDLVVVAESCXVDEEDRAALR

SEQ ID NO. 84 (BNL8, 4k)

STVTEKDIRPEEEVYQCCDLEPEARKVITALTERLYVGGPMHNSKGDLCGYRRCRASGVYTTSFGN TLTCYLKASAAIRAAGLRDCTMLVCGDDLVVIAESDGVEEDNRALXA

SEQ ID NO. 86 (BNL12,41)

STVTEKDIRVEEEIYQCCDLXPEARKAISALTEXLYLGGPMYNSKGELCGYRRCRASGVYTTSFGN TVTCYLKATAATRAAGLKDCTMLVCGDDLVVIAESEGVEEDSOPLRA

SEQ ID NO. 88 (EG81, 4m)

STVTERDIRVEEEVYQCCDLEPEARKAISALTERLYVGGPMFNSKGDLCGYRRCRASGVYTTSFGN TLTCYLKATAATRAAGLKDCTMLVCGDDLVVIAESDGVDEDRRALQA

SEQ ID NO. 90 (VN13,7a)

STVTERDVQTEHDIYQCCKLEPAARTAITSLTDRLYXGGPMXNSKGQACGYRRCRASGVLTTILAN TLTCYLKAQAACRAAGLKDFDMLVCGDDLVVISESLGVSEDTSALRA

SEQ ID NO. 92 (VN4,7c)

STVTERDIXTEHDIYQCCQLDPVARKAITSLTERLYCXGPMMNSRGQSCGYRRCRASGVLTTSLGN TLTCYLKAQAACRAAKLKNYDMLVCGDDLVVIAESGGVSEDVDALRA

SEQ ID NO. 94 (VN12,7d)

SSVTERDIRTEHDIYQCCQLDPVARKAITSLTERLYCGGPMYNSRGQSCGYRRCRASGVFTTSLGN TMTCYLKAQAACRAXKLKNFDMLVCGDDLVVIAESGGVPEDAGALRV

SEQ ID NO. 96 (FR1,9a)

STVTGRDIRTEXDIYLSCQLDPEARKAIKSLTERLYVGGPMYNSKGQLCGQRRCRASGVLPTSMGN TITCFLKATAACRAAGFTDYDMLVCGDDLVVVTESAGVNEDIANLRA

SEQ ID NO. 98 (NE98, 10a)

STVTEQDIRVELSIFQACDLKDEARRVITSLTERLYCGGPMFNSKGQHCGYRRCRASGVLPTSFGN TITCYIKAKAATKAAGIKNPSFLVCGDDLVVIAESAGIDEDKSALRA

SEQ ID NO. 100 (FR14,11a)

STVTERDIRTEESIYLSCQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGN TMTCYIKAKAACKAAGIVDPVMLVCGDDLVVISESKGVEEDQRDLRV



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Fig.3P

Figure 3 - continued

SEQ ID NO. 102 (FR15,11a)

STVTERDIRTEESIXXACQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGN TMTCYIKAXAACKXAGIVDPVMLVCGDDLVVISESKGVEEDQRDLXX

SEQ ID NO. 104 (FR19,11a)

 ${\tt MSTNPKPQRQTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRVGVRATRKTSERSQPRGRRQPIPKVRRTTGR}$

SEQ ID NO. 106 (FR19,11a)

STVTERDIRTEESXYLACQLPEEARKAIKSLTERLYVGGPMENSKGQACGYRRCRASGVFTTSLGN TMTCYIKAKAACKAAGIVDPVMLVCGDDLVVISESKGVEEDQRDLRX



Fig. 4A core/El amino acid alignment



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solate	Type	SEQ	
		QI	1 50
HCV-1	la		MSTNPKPQKKNKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATR
HCV-J	1p		
BNL1	1q	2	R-TXXXXXX
BNL2	1d	9	R-TXX
CAM1078	1e	10/60	R-TA-
FR2	1£	12	R-TR-T
FR16	19	99	R-TII
HC-J6	2a		R-TR-T
HC-J8	5 p		R-TR-T
CH610	2 _C		
NE92	2 q		R-TR-T
BNL3	رع 9	14	K-TR-T
FR4	JĘ	18	R-TP-
FR13	2k	92	R-TXXXCX
E B1	3а		R-TIC
NZL1	39		LR-TI
HCV-TR	3p		LRQTLN
GB358	4 c		R-TM
DK13	4 d		R-TM
CAM600	4 e		R-TMM
GB809	4e		L-R-TM
HPCCOREEZA	č Þ		9
HPCCOREZB	4.5		
HPCCOREZC	42		
GB724	5 7		
BNL7	4 X	28	R-TR-T
BE95	5a		
HK2	6а		LR-TT
VN13	7 a	46	IR-T
VN4	7c	44	IR-TII
VN12	Jq	48	LR-T
FR1	9a	42	IR-TM
NE98	10a	20	LR-TX
FR19	11a	104	ROTV





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Isolate	HCV-1 HCV-J	BNL1 BNL2	CAM1078	FR2 5016	HCJ6	HCJ8	CH610	NE92	BNL3	FK4 FB13	En I	N21.1	HCV-TR	GB358	DK13	CAM600	GB809	BNL7	HPCCOREEZA	HPCCOREZB	HPCCOREZC	GB724	BE95	HK2	VN13	VN4	VN12	FRI	NE98	FKIS





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Fig. 4C	101 RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADIMGYTPINGAPIGGAARA		N			ù-SN	ı	^^NN	VV	NNN	1	^-XXX	: !	\n\-\x\\n\	AA	/ A A	4 \(\tau -	^\n-\n\n\n\n\n\n			\ \ \	~^-	N	NNK		HXXXNNNN	N	NH	VI-G	
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Isolate	HCV1	HCV-J	BNL1	BNL2	CAM1078	FR2	FR16	HC-J6	HC-J8	CH610	NE92	BNL3	FR4	FR13	HCV-TR	GB116	DK13	CAM600	GB809	622	GB549	GB438	BNL7	BE95	HK2	VN13	VN4	VN12	FRI	NE98





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Fig. 4D	151 200	vrvledgvnyatgnlpgcsfsifllallscltvpasa <mark>y</mark> qvrnstgl					- FIII-I-I-I-N-N-	·-^	>== 7)-A	\X-\-\-\-\-\-\-\-\-\-\-\-\-\-\-\-\-\-\-	-XI^-II	\\n-\n-\\		{^	-TXNT	LEWTS	I-TS	<u> </u>	1	OM-180	- T ^ V	AS	SXN	ITNNYAS	IGVNYAS	AVI	VHYH-TS	SIXIIOI	QHYAS	INYVS-	S.I I X II - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	4 1
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	Isolate	HCV1	HCV-J	BNL2	FR2	FR16	HC-J6	HC-J8	SB3	NE92	BNL3	FR4	BNL4	BNL5	BNL6	FRI3	i	HCV-TR		GBBU9-4 71	31102	GB215	GB358	DK13	CAM600	CB809-2	CAMG22	CAMG27	GB549	GB438	DNL/ BNI 8	o TNE	BNL10







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1 4 4 4 7 7 7 8 9 9 9 0 8 9 8 8 8 8 9 9 9 9 9 9 9 9 9
BNL11 BNL12 BE95 BE100 HK2 VN4 VN12 FR1





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VAMTPTVATRD LL-A-N M-LL-VKX MXLL-VKX
VA VREGNASRCWVAMTPTVAMTRD S-FL-A-N D-HLMXLL-A-I IIMXLL-A-I EKV-TPLNK EQIPVS-NVQQ ENDNGTLHIQV-NVQQ ENDNGTLHIPVS-NVSQ ELQKIVSQ ENCOTTPVS-NVSQ ENCOTTVSQ ENCOTT
V3 CV REGNASRCW CENDACTION
PNSSINYEAADAILHTPG S
V1 XHWTNDCPNSSIR XH
10 ID
F V 11111110101010101010101010101010101010
Isolate HCV-1 HCV-J BNL1 BNL2 FR2 HC-J6 HC-J6 HC-J6 HC-J8 CH610 S83 NE92 BNL3 FR13 BNL5 BNL5 BNL5 BNL5 BNL5 GB809-4 Z1 GB809-2 CAMG22 GB815 GB815 GB815 GB816 GB815 GB816 GB817 BNL3 BNL3 BNL3 BNL110
4. H





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LAPI	ITPVAVS	QILSAPS	1	LL-DAMLLVDDR-TH-VI-IPN	LQASLVPN	LLSASL-VQN	LS-NFETMLIKAELPVSL-VPN	2411S-G
40					44	48	42	52
41	42	5a	5a	6 a	7c	7d	9a	10a
BNL12	GB724	BE95	BE100	HK2	VN4	VN12	FRI	NE98



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SVFLVGQLFTESPRHWT	-AIMIAA-VVIV -AAGAMMIGA	
V4 State	VAIMIAA-VVIVEH-HFMAARQAF-AART	
YVGDLCG	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	
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71		
RHIDLLVGSATLCVXA-FV	I - A F - I - A F - I - A F - I - A - A - A - A - A - A - A - A - A	CAHHAAAAAAA
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	₽'	0,146
Isolate HCV-1 HCV-J BNL1 BNL2 FR2 HC-J8 CH610 S83 NE92 BNL3 FR4 BNL3	BNL6 FR13 BR36 HCVTR 24 GB809- C1 GB116 GB215 GB215 GB215	D 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
ISOJAT HCV HCV BNL1 BNL2 HCJER2 HCJER2 HCJER2 HCJER4 S83 NE92 BNL3 FR4 BNL3 BNL3	BNL6 FR13 BR36 HCVTI 24 GB80 C1 GB11 GB21 GB35 GB35 GB35	CAMB GB80 CAMG; CAMG; CAMG; GB54 GB43 GB43 BNL7 BNL9 BNL9 BNL9 BNL9 BNL9 BNL9 BNL1



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			5	2/:	74			
LSA-LMSVVMASGAM0	VDA-LESFVMAVGAMO	A	1 1	S1	AST-V-GF-K-V-IMA-AFMGLLRM-OV	GI	II	ALXG
40						48		
41	42	5a	5a	6 a	7c	7d	9 a	10a
BNL12	GB724	BE95	BE100	HK2	VN4	VN12	FR1	NE98

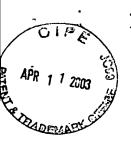


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SEQ	٠ ر		マ	ထ	12						16																				30	32	34	36	38	40
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Isolate	HCV-1	- \	BNL1	BNL2	FR2	HC-J6	HC-J8	CH610	S83	NE92	BNL3	FR4	BNL4	BNLS	FR13	BR36	HCVTR	54	GB809-4	21	GB116	GB215	GB358	DK13	CAM600	GB809	CAMG22	CAMG27	GB549	GB438	BNL7	BNT8	BNL9	BNL10	_	BNL12



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7932	CICCACAGICACIGAGAGCGACAICCGIACGGAGGAGGCAAICIACCAAI	AGATAT	NAT	ATGTC	TATA	GTATGTCATG-	AGAGCTTAAT-CA	NATTTT	NNNNNNNTTGTCRTT	ACAA-GTT-CA-GG	ACGGAA-A-A-A-A-AT-CATGG	GAATAA-NTT-CAGG	ACAGTAA-ATT-CATGG	AG-GAA-GCT-CT-G	AT-CG-TT-TG-	AGGA-G-ATT-CA-TG-TGG	ATACAGA-GGTAA-AGA	TTACATA-GAGA-G	TTTACAGTA-GGTAA-A-AAA
SEQ ID				53	55	57	19	63	6 3			69	71	73	11	79			81
Type	la	1p	1b	1d	1d	1d]e	lf	lg	2a	2р	دع 9	7.F	2h	7, X	77	3a	3p	3g
Isolate	HCV-1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	T9	PAK64

Fig. 5A NS5B nucleotide alignment



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Isolate	Type		
	! !	ΠD	7981
GB48	4 C		-CA-AGA-GGTCAGG
GB116	4 C		
GB215	4 C		ACA-AAA-GGTCAG-A
GB358	4 c		-CA-AGA-GGTCAGG-GT-
GB809	4 e		AAGGTCA-AAAAAAAA
GB549	4 q		CAGTA-GCA-AG
BNL8	<u>4</u> አ	83	-ACA-AGA-GC-CA-AGG
BNL12	41	85	-GA-AGA-GGTCA-AG
EG81	4 m	87	-ACAGA-GGTCA-GGTC-
CHR18	5a		-TCACATAATGTAT
VN13	7a	89	
VN4	7c	91	CC
VN12	7d	93	-CGC-TC-TAC-C-AC-C
FR1	9a	95	B-G-G-CA-
NE98	10a	97	CAGA-GGTAACTTT-C
FR14	11a	66	AABBAA
FR15	11a	101	
FR19	11a	105	GTATG



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,	8031									5	7/	74							
7982	TGACCTCGACCCCCAAGGGGGGGGGGGGAAGAAGAAGAAGA	T-G-CGB-CCDB-CCD			 		bm		G-CG-C				ACC-GAGGGACTAC-CAI-GI-	ACC-GAGADDCG-ACC-GAG-AB A	-TCATCC-GAGG-GA-CMAC-1AI-G	GCC-GAGG-GGACTA-A-A-A-A-A-A-A-A-A-A-A-A-A-A-A-A		1C1C	AT-979BBBBBBBB
ΩĬ				53	55	57	61	63	6 3			69	71	73	77	79			81
1	la	1p	1p	1d	1d	1q]e	1£	1g	, c	9 2	رع 4	5£	2h	7, 7,	7.7	3а	3p	39
	HCV-1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	T9	PAK64

Type SEQ

Isolate



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			AATAT-CCG	AAAT-CTG	AGCCG	AAIGAICCGA	TTT-CCG	AAAATCCG	AAATCCG	-GTAACGA	AGACACAG-	AAATT-CA-	-AGAAA	GAAAA	TG	GAAATAGG	GAATA-	GAAA-
7987	· · · · · · · · · · · · · · · · · · ·	-9-99	99	-9-99	-G-	-G-	·99	GRG	TGGBG-G-	CA-TGTT-GC-GTG-G-	-CA-GT-GGGC	1	-CCC-AT-ATGGT	CCCC-GAG-G-	CCA-GGA-G-C-TA-GAG	CC-AT-GCCTGAAG-G-	CC-AT-GCC-GAAG-G-	CC-AT-GCC-GAAG-G-
SEQ TD	•						83	85	87		89	91	93	95	97	99	101	
Type	4°C	. 4c	4°C	4°	4 e	4 g	4 X	41	4m	5a	7a	7c	7d	9a	\circ	$\overline{}$	11a	$\overline{}$
Isolate	GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19



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	8032	AGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAAAAAAGAAAAAAAA	C							-\frac{4}{2}\frac{4}{2}\frac{1}{2}\f		ローンシーーは - ンりなう	- 1	DI D V) D				C C C C C C C C C C C C C C C C C C C))A-CAGC-A	C G CA-CATCA-GTACAGT-ACTCC-G
SEQ					53	55	57	61	63	29			69	71	73	77	79	ı		<u>a</u>
Type		la	1 p	1b	1q	1d	1d	le	1£	1g	رع م	2p	2e	2£	2h	2 k	21	3a	<u>ج</u> ج) (S
Isolate		HCV-1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	HC-J8	BNL3	FR4	BNL5	FR13	FR18	T1	19	DAK64





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Usolate ISolate GB48	> 000000000000000000000000000000000000	80 80 80 80 80 80 80 80 80 80 80 80 80 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	~ ~	01 05	AACGCGA-GGAACAGC-AACCGC AACGCGA-GGAACAGC-ACCGC





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	8082	yJwjjjjjy				P OT						シージールーンーーンー	-CT		-AC-AAAA			DT	3C-TAGT-CCATG	
ഗ	IDI							83	85	87				93				0		
Type	1	4 C	4 C	4 C	4c	4 e	4 g	4 7	41	4m	5 a	7a	7c	7d	9a		11a	_		
Isolate		GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19	



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Isolate	Type	SEQ	
		Π	8132
HCV-1	la		CCCTCACTTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGCTC
HCV-J	1b		ATACTGALG
BE90			
BNL1		53	AA-BGA
BNL2		55	I-GAAG
FR17		57	TT-GAA
CAM1078		61	TAT
FR2		63	TB
FR16		29	TBBB
HC-J6			AAG
HC-J8			
BNL3		69	T UTUT
FR4		71	- -
BNL5		73	TA
FR13		77	D-GBBD
FR18		79	TG-GAATTCA
$_{ m T1}$	3a		
T9	35		
PAK64	3g	81	G





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Isolate Type SEQ										(64 <i>i</i>	74	ļ							
ate Type 66 40 40 69 99 44 60 69 69 69 69 69 69 69 69 69 69 69 69 69			-GCATCACTATCAAGG	-GTCATCACTATCAGG-	-GTCATCACATCA-GGT	-GCGTCACTATCAG	-GC-TTCAATCA-GTG	AGTTCGTTG-TAC-A-G	-GGATCAT-TAT-AG	-CTC-TACCTACCA-GTCA	-CCACCTACCAGCG	-GAA	-GT-GAT-AGACATCG	-ATT-GAA-AAGA-GAA	-AC-GT-AGT-A-G	AT-C-GAACCCTCA	CTAAATACCAATC-	TATAAAGTAA	TYT	-GTAAAGTAAT
ል እስወወወ (1 8 ከ በ													89	91	93	95	97	66	0	0
Isolate GB48 GB116 GB215 GB358 GB358 GB358 GB349 GB358 GB349 G	Type	7 47 -	4 c	4 c	4 c	4c	4 e	49	4 k	41	4 m	5a	7a	7c	7d	9a		$\overline{}$	11a	11a
	Isolate		GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FRI	NE98	FR14	FR15	FR19



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8231 CAGGACTGCACCATGCTGTGGCGACGACTTAGTCGTTATCTGTGA CAGGACTGCACCATGCTGTGGCGACGACTTAGTCGTTATCTGTGA	
SEQ 1D 1D 53 57 63 67 77 79	
Type 11 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13	a
Isolate HCV-1 HCV-J BE90 BNL1 BNL2 FR17 CAM1078 FR2 FR2 FR16 HC-J8 BNL3 FR4 BNL5 FR4 T1 T1 T9	• > :



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									6	6/	74							
(023T																	
(S)	JJJJUHHH)	>		9 9)B		-I-J	ATGAT-ACCATTT	I-GCD			BCCGGTG)
IDK							83	85	87		83	91	93	95	97	99	101	105
77	4 C	4 C	4c	4 C	4 e	49	4 7	41	4 m	5a	7a	7c	7d	9a			11a	_
	GB48	GB116	GB215	GB358	GB809	GB549	BNL8	BNL12	EG81	CHR18	VN13	VN4	VN12	FR1	NE98	FR14	FR15	FR19

Isolate



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AAGCGCGGGGTCCAGGAGGACGCGGCGAGCCTGAGAGCC --AAC--SEQ ID 53 57 61 63 69 71 73 77 81 Type 33377776 333777776 33377776 33377776 33377776 FR17 CAM1078 Isolate FR2 FR16 HC-J6 HC-J8 BNL3



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Isolate GB48 GB116 GB215 GB358 GB809 GB549 GB549 GB549 GB549 GB549 VN13 VN13 VN13 VN13 VN13	Н 4444444444 Т 7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SE SE SE SE SE SE SE SE SE SE SE SE SE S	Fig.5N 232 ATC-AGAAACGAGCATC-TGAAACGAGCATC-TGAAACGAGCATC-TGAAACGAGCATC-TGTAACGAGCATC-AGTAACGAGCATC-AGTAACGAGCATC-AGTAACGAGCATC-AGTT-CCAACCATC-AGTT-CCAACCTTACG-CTAAATTACG-CTAAATT
FR15	नं न	101	GAAAGCA-CGAGAAC
FR19		105	AAGGCAACGAGAACNT-

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e SEQ ID 54 56 64 68 70 72 74 78 80													
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Isolate HCV-1 HCV-J 2TY4 BNL1 BNL2 FR17 CAM1078 FR2 FR2 FR2 FR2 FR16 HC-J6 HC-J8 ARG8 NE92 BNL3 FR4 BNL5 FR13 FR4 BNL5 FR13 FR4 BNL5 FR13 FR14 BNL5 FR13 FR19 FR13 FR19 FR13 FR19													

Fig.6A NS5B amino acid alignment



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GB48 GB116 GB215 GB215 GB215 GB358 GB809 CAMG22 GB438 CAR1/501 EG13 BNLB BNLB BNL12 EG81 BNL12 EG81 BNL12 EG81 BNL12 EG81 BNL12 EG81 BNL12 EG81 BNL12 FR14 FR15 FR15	



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Fig.6C	2695	2./ RASGVLTISCGNTLTCYIKARAACRAAGT.ODCTMI.VCGDDI.MYTCF		ι ! ! α	````````\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\				\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\			-C	^		-II'K	-TVTK	·X11-	·		ABNDDE	TGTWY	FTT		
SEO	ID							29		89					70	72	74	78	80					82
Tvpe	1	la	1b	10	1q	1q	1q	1e	1£	1g	ر م م	2p	20 C	2d	2e	2£	2h	7 7 7	21	3a	Зa	3a	3b	3g
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116 116 117 117 117 117 117 117 117	ENLS BNL12 EG81 EG81 BE95 CHR18 VN13 VN13 VN12 FR1 FR14 FR15



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745	AG	TA	VT	NE	EV	-XEV	-V-T	IE-XXPS		-Q-TEERN	-Q-NEERN	-Q-TEERN	1	-Q-AEERNV	-TE	R-ENN	-Q-TEERNV	i	i		-CER-A	-CX-D-EDRAALR
SEQ ID								64						72								82
Type	la	1b	1b	1q	1d	1 1	1e	1	1g	رم ھ	2 p	2d	2e	5.£	2h	2k	21	3a	3a	3a	3p	39
Isolate	HCV-1	HCV-J	BE90	BNL1	BNL2	FR17	CAM1078	FR2	FR16	HC-J6	\vdash	NE92	BNL3	FR4	BNL5	FR13	FR18	BR34	BR36	BR33	T9	PAK64
1.6E																						



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-DEKRP-G- -DEKRA-G- -DEKRA-GV -DEKRA-G-	1 1	ERA-	-GERA	KQA	EPXTX-P	l l		D	-0-THE	H	-LSTSA	S	1	H	—— 不	-KEQ	2 -KEORD-	-KE
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1.6F																		